

40

Access DB# 40349

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: Chen - Joly
 Searcher Phone #: 308-4501
 Searcher Location: Bited Lit.
 Date Searcher Picked Up: 4/17/01
 Date Completed: 4/25/01
 Searcher Prep & Review Time: _____
 Clerical Prep Time: 5 mi
 Online Time: 8 mi

Type of Search

NA Sequence (#) 1
 AA Sequence (#) 1
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr.Link _____
 Lexis/Nexis _____
 Sequence Systems ABS502/Compugen 1
 WWW/Internet _____
 Other (specify) _____

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

40344

From: Chan, Christina
Sent: Tuesday, April 17, 2001 12:05 PM
To: Kemmerer, Elizabeth; STIC-Biotech/ChemLib
Subject: RE: rush seq search req

[Handwritten signature]

~~Please rush.~~ **Thanks Chris**

Chris Chan
TC 1600 New Hire Training Coordinator and SPE, 1644
CM 1, Room 9B19
308-3973

CRFE

-----Original Message-----

From: **Kemmerer, Elizabeth**
Sent: Tuesday, April 17, 2001 12:05 PM
To: Chan, Christina
Subject: rush seq search req

Hi, Christina-
Please approve the following for an overdue amended from Garnette Draper's docket. Thanks!

STIC:
Please rush a regular + interference search of SEQ ID NOS: 25 and 26 for 08/741095. Thanks,

Elizabeth (Betsy) Kemmerer
Art Unit 1646
308-2673
CM1-10B17

This search was run on the machines we identify as Compugen1, abss03, abss04, or abss05. The databases on these machines are exactly the same as those on the other machines. However, for searches run on the listed machines, two sets of results are now generated when the Pending Nucleic Acid and/or Pending Amino Acid databases are searched. The Pending databases have been split into two parts to reduce the amount of time required for their daily update.

Searches run against the Nucleic Acid Pending database will produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database will produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 14:12:42 ; Search time 71.66 Seconds

(without alignments)
4618.460 Million cell updates/sec

Title: US-08-741-095B-25

Perfect score: 881
1 cctgagcagatgagcctcct.....ccacagactgcaccccca 881

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_36:*

- 1: /cgnl_8/gcgdata/geneseq/geneseqn/NA1980.DAT:*
- 2: /cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT:*
- 3: /cgnl_8/gcgdata/geneseq/geneseqn/NA1982.DAT:*
- 4: /cgnl_8/gcgdata/geneseq/geneseqn/NA1983.DAT:*
- 5: /cgnl_8/gcgdata/geneseq/geneseqn/NA1984.DAT:*
- 6: /cgnl_8/gcgdata/geneseq/geneseqn/NA1985.DAT:*
- 7: /cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT:*
- 8: /cgnl_8/gcgdata/geneseq/geneseqn/NA1987.DAT:*
- 9: /cgnl_8/gcgdata/geneseq/geneseqn/NA1988.DAT:*
- 10: /cgnl_8/gcgdata/geneseq/geneseqn/NA1989.DAT:*
- 11: /cgnl_8/gcgdata/geneseq/geneseqn/NA1990.DAT:*
- 12: /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:*
- 13: /cgnl_8/gcgdata/geneseq/geneseqn/NA1992.DAT:*
- 14: /cgnl_8/gcgdata/geneseq/geneseqn/NA1993.DAT:*
- 15: /cgnl_8/gcgdata/geneseq/geneseqn/NA1994.DAT:*
- 16: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:*
- 17: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT:*
- 18: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:*
- 19: /cgnl_8/gcgdata/geneseq/geneseqn/NA1998.DAT:*
- 20: /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	881	100.0	881	17	T40048 Human tumour necro
2	879.4	99.8	1704	19	V4509 Human TNF receptor
3	879.4	99.8	1704	20	V83763 Human tumour necro
4	873	99.1	1724	18	T51737 Human hepes simpl
5	873	99.1	1724	20	X25512 Herpes virus entry
6	858.4	97.4	927	19	V44852 Hepesvirus entry
7	858.4	97.4	927	20	X87265 CDNA clone encodin
8	732.4	83.1	1834	21	Z94198 Membrane-bound her
9	688.8	78.2	1929	21	Z94195 Soluble herpesvitu
10	671.4	76.2	1596	21	Z94196 Soluble herpesvitu
11	555.8	63.1	2313	21	Z94197 Soluble herpesvitu
12	342.2	38.8	2692	19	V34510 Human TNF receptor

13	306.2	34.8	723	17	T40049 Human tumour necro
14	239.4	27.2	2637	19	V34511 Human TNF receptor
15	233.4	26.5	405	17	T40050 Human tumour necro
16	62	7.0	2393	12	O10907 40KD TNF inhibitor
17	60.4	6.9	705	19	V41549 Human soluble tumo
18	60.4	6.9	705	19	V19802 Human tumour necrosi
19	60.4	6.9	705	20	V81733 Tumour necrosis in
20	59.6	6.8	1691	16	T05443 BamP delta53 nerv
21	58.6	6.7	1004	13	O21176 Human CD40 antigen
22	58.6	6.7	1004	14	O47341 CD40 coding sequen
23	58	6.6	705	21	Z45760 DNA encoding a K12
24	58	6.6	705	21	Z45762 Wild type N-terma
25	58	6.6	1557	15	O45225 Sequence encoding
26	58	6.6	1640	12	O10990 Partial sequence o
27	58	6.6	1641	14	O49931 TNF-R CDNA. Homo
28	58	6.6	2224	16	O89544 p75 Tumour Necrosi
29	57	6.5	822	21	Z55527 Canine CD40 CDNA c
30	57	6.5	822	21	Z55528 Canine CD40 CDNA c
31	57	6.5	1004	10	N90617 Human CDNA. N9061
32	57	6.5	1004	17	T14706 Human CD40 antigen
33	57	6.5	1004	19	V63454 Human CD40 antigen
34	57	6.5	1004	20	Z23432 Human CD40 DNA. H
35	57	6.5	1004	20	Z40936 Human CD40 encodin
36	57	6.5	1004	20	V81198 Human CD40 antigen
37	57	6.5	1004	21	Z47769 Human CD40 nucleot
38	57	6.5	1425	21	Z55525 Canine CD40 CDNA.
39	57	6.5	1425	21	Z55526 Canine CD40 CDNA c
40	56.4	6.4	705	21	Z45759 DNA encoding a K10
41	56.4	6.4	705	21	Z45761 DNA encoding a K10
42	55.4	6.3	1004	20	Z20296 CD40 CDNA. Unden
43	51	5.8	765	21	Z55529 Canine mature CD40
44	51	5.8	765	21	Z55530 Canine mature CD40
45	50.8	5.8	1641	15	O45224 Sequence encoding

ALIGNMENTS

RESULT 1	
T40048	
ID T40048 standard; cDNA: 881 BP.	
XX	
AC T40048:	
XX	
DT 30-JUN-1997 (first entry)	
XX	
DE Human tumour necrosis factor receptor cDNA.	
XX	
KW Human; tumour necrosis factor; TNF; receptor; treatment;	
KW activation; inhibition; identification; agonist; antagonist;	
KW stimulation; T cell; differentiation; mediation; immune;	
KW antiviral; response; regulation; growth; protection; HIV;	
KW radiation; Chlamydia; infection; immunodeficiency; virus;	
KW autoimmune disease; inflammation; septic shock; malaria;	
KW cachexia; B cell; cancer; graft; host; reaction; rejection;	
KW prevention; apoptosis; cytotoxicity; hybridisation probe;	
XX detection; antibody; reagent; ss.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT CDS	..860
FT	/*tag= a
FT	sig_peptide 9..122
FT	/*tag= b
FT	mat_peptide 123..857
FT	/*tag= c
FT	/product= tumour_necrosis_factor_receptor
PN W09634095-A1.	
XX	
PD 31-OCT-1996.	
XX	

27-APR-1995; 95MO-US050508.
27-APR-1995; 95MO-US050508.
(HUMA-) HUMAN GENOME SCI. INC.
Gentz R, NI J, Rosen CA;
WPI: 1996-497627/49.
P-PSDB; W05809.
New nucleic acid encoding a human tumour necrosis factor receptor -
useful for treatment of auto-immune diseases etc., in diagnosis and
for drug screening
Claim 10; Page 47; 73pp; English.

Query Match	100.0%	Score 881;	DB 17,	Length 881;
Best Local Similarity	100.0%;	Pred. No. 1.4e-214;		
Matches 881; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

Db	481	aggaataccctctgttgcataggaactgcgcccccgcggggaacctctctctccaatagggaacctctggagg	540
QY	541	aatgtcagaccacagagccaagtgcagctgtgcctgtgtgcacgaagcccggaagctctgggaacca	600
Db	541	aattgcagcacaccagagccaagaatgcagctgtgcctgtgtgcacgaagcccggaagctctgggaacca	600
QY	601	gtcccaattgggtatctgtgtgttctcttcacagggaagccctgcatactgatactgtttgtctcca	660
Db	601	gtcccaattgggtatctgtgtgttctcttcacagggaagccctgcatactgatactgtttgtctcca	660
QY	661	caattgtgcctcaatacatatgtgtgcgaagaagaaagcccaaggggtgtacgtatgcacaagttga	720
Db	661	caattgtgcctcaatacatatgtgtgcgaagaagaaagcccaaggggtgtgtacgtatgcacaagttga	720
QY	721	tcgtctccgtccacagtcggaagaagacagaggagcagaaggtgtgaagccacagtcacattggaagccc	780
Db	721	tcgtctccgtccacagtcggaagaagacagaggagcagaaggtgtgaagccacagtcacattggaagccc	780
QY	781	tgcagagcccccctccggaagctcacacacggtgtgcctgtgtggagagacaatactcctcatltaacg	840
Db	781	tgcagagcccccctccggaagctcacacacggtgtgcctgtgtggagagacaatactcctcatltaacg	840
QY	841	ggagagagcccaaacacacatgcatacccaagatcttgcaccccga	801
Db	841	ggagagagcccaaacacacatgcatacccaagatcttgcaccccga	801

XX	RESULT	2
XX	V34509	
XX	ID	V34509 standard; cDNA; 1704 BP.
XX	AC	V34509;
XX	DT	25-SEP-1998 (first entry)
XX	DE	Human TNF receptor related (TR2) gene.
XX	XX	ds; human; tumour necrosis factor; TNF; herpes simplex virus;
XX	KW	aberrant cell survival; radiation therapy; lymphocyte proliferation;
XX	KW	immune deficiency syndrome.
OS		Homo sapiens.
XX		
XX	FH	Location/Qualifiers
FT	CDS	265..1116
FT		/*tag= a
FT		/product= "TR2 protein"
FT	sig_peptide	265..372
FT		/*tag= D
FT	mat_peptide	373..1116
FT		/*tag= C
XX		
XX	PN	W09818824-A1.
XX	XX	
XX	PD	07-MAY-1998.
XX	XX	
XX	PE	30-OCT-1996; 96MO-US18540.
XX	PR	30-OCT-1996; 96MO-US18540.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.
PI		
XX	PI	Gentz RL, Hurle MR, Lyn SDP, Nl J, Rosen CA;
XX	DR	WPI; 1998-272139/24.
XX	DR	P-PSDB; W460045.
XX		
PT		Nucleic acid encoding TR2 tumour necrosis factor family receptor -
PT		and its splice variants; useful for diagnosis and treatment of
PT		diseases involving abnormal cell survival or death, e.g. herpes
XX		simplex infection
XX		

PS Claim 2; p86-88; 151pp; English.

CC The human tumour necrosis factor (TNF) receptor related protein (TR2) is
 CC a member of the TNF family and displays considerable homology to murine
 CC CD40. It can be used in soluble forms to treat herpes simplex virus
 CC infection and TR2 proteins (or their agonists or antagonists) are used to
 CC treat disease associated with aberrant cell survival. Agonists may also
 CC be used to protect against the effects of radiation therapy and to
 CC stimulate lymphocyte proliferation and differentiation in patients
 CC infected by human immune deficiency syndrome.

XX Sequence 1704 BP; 343 A; 529 C; 504 G; 328 T; 0 other:

Query Match 99.8%; Score 879.4; DB 19; Length 1704;

Best Local Similarity 99.9%; Pred. No. 4.3e-214;

Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgaggcatgagagcctctctgagagctgggggctctctccctctgagatccacccacagaa 60
 DB 257 cctgaggcatgagagcctctctgagagctgggggctctctccctctgagatccacccacaa 316
 QY 61 ccgagcgtcttgagagctgctgtctgtatctcaactctctggagagccctctgtaagcccaag 120
 DB 317 ccgagcgtcttgagagctgctgtctgtatctcaactctctggagagccctctgtaagcccaag 376
 QY 121 cctgcgcctctctgag 180
 DB 377 cctgcgcctctctgag 436
 QY 181 gtcagggtatcgtgtgaaag 240
 DB 437 gtcagggtatcgtgtgaaag 496
 QY 241 gccctccag 300
 DB 497 gccctccag 556
 QY 301 tgtgtgag 360
 DB 557 tgtgtgag 616
 QY 361 tgtgtgag 420
 DB 617 tgtgtgag 676
 QY 421 gccgaggtatcag 480
 DB 677 gccgaggtatcag 736
 QY 481 aggag 540
 DB 737 aggag 796
 QY 541 aatgtgag 600
 DB 797 aatgtgag 856
 QY 601 gctcccaactggtatggtgttctctcagagagagagagagagagagagagagagagagagag 660
 DB 857 gctcccaactggtatggtgttctctcagagagagagagagagagagagagagagagagagag 916
 QY 661 caggtgag 720
 DB 917 caggtgag 976
 QY 721 tctgtctcag 780
 DB 977 tctgtctcag 1036
 QY 781 tgcag 840
 DB 1037 tgcag 1096

QY 841 ggaag 881
 DB 1097 ggaag 1137

RESULT 3

ID V83763 standard; cDNA; 1704 BP.

XX V83763;

DT 17-MAR-1999 (first entry)

XX Human tumour necrosis factor receptor-like 2 protein coding sequence.

DE Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis;

KW systemic lupus erythematosus; idiopathic thrombocytopenic purpura;

KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;

XX insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;

XX artherosclerosis; viral infection; ss.

PN WO9851346-A1.

XX 19-NOV-1998.

XX 12-MAY-1998; 98MO-US09744.

XX 12-MAY-1997; 97US-0046249.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Harrop JA, Holmes SD, Reddy MP, Truneh A;

XX WPI; 1999-059689/05.

XX P-PSDB; W87591.

PT Method of treating pathological condition - comprises administering

XX tumour necrosis factor-2 antibody to patient

XX disclosure; Page 26-27; 35pp; English.

CC This sequence encodes the human tumour necrosis factor (TNF)

CC receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can

CC be used in the method of the invention to treat pathological conditions.

CC Thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,

CC psoriasis, inflammatory bowel disease, insulin-dependent diabetes

CC mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic

CC dermatitis, cancer, e.g. lymphomas and leukaemias, atherosclerosis and

CC viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody

CC is also used to monitor and diagnose abnormalities in TR-2 function,

XX production or metabolism.

SO Sequence 1704 BP; 343 A; 529 C; 504 G; 328 T; 0 other:

Query Match 99.8%; Score 879.4; DB 20; Length 1704;

Best Local Similarity 99.9%; Pred. No. 4.3e-214;

Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgaggcatgagagcctctctgagagctgggggctctctccctctgagatccacccacagaa 60
 DB 257 cctgaggcatgagagcctctctgagagctgggggctctctccctctgagatccacccacaa 316
 QY 61 ccgagcgtcttgagagcgtgtctgtatctcaactctctgagagccctctgtaagcccaag 120

```

Db 317 cccagctcttgagcgtgctgtatctcaacctctctggagagccctctgtaagcccccag 376
QY 121 ctctgcctctctgcaagagagacagtaaccagtggtctccagatgtctgcccagaatgca 180
Db 377 ctctgcctctctgcaagagagacagtaaccagtggtctccagatgtctgcccagaatgca 436
QY 181 gtccaggtatctgtgtaagagagcctgagggagctgacgggacagatgtgtgaacct 240
Db 437 gtccaggtatctgtgtaagagagcctgagggagctgacgggacagatgtgtgaacct 496
QY 241 gccctccagacactatctgcccacactcaatgacctgaagcaagtgtctgcaatgcca 300
Db 497 gccctccagacactatctgcccacactcaatgacctgaagcaagtgtctgcaatgcca 556
QY 301 tctgtgtaaccagacatgtggctctgagcgagagccggaactgtctccagagacagacgcg 360
Db 557 tctgtgtaaccagacatgtggctctgagcgagagccggaactgtctccagagacagacgcg 616
QY 361 tctgtgttgtaagccagagcactctgtcaatgctccagagagcgagacactgagcgct 420
Db 617 tctgtgttgtaagccagagcactctgtcaatgctccagagagcgagacactgagcgct 676
QY 421 gccgcgttaacgacacactccagcccgagcgagaggtgacagaaaggagagacccagatc 480
Db 677 gccgcgttaacgacacactccagcccgagcgagaggtgacagaaaggagagacccagatc 736
QY 481 aggaacacctgtgtcaagaactgcccccgaggagccttctcccaatggagacctgtgag 540
Db 737 aggaacacctgtgtcaagaactgcccccgaggagccttctcccaatggagacctgtgag 796
QY 541 aatgtacagacacagacaaagtgtgagctgtgtgtgtaagagcgagcgtgagacagca 600
Db 797 aatgtacagacacagacaaagtgtgagctgtgtgtgtaagagcgagcgtgagacagca 856
QY 601 gtcccaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
Db 857 gtcccaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 916
QY 661 cagttgtgctaatcatatgtgtgtaaaagaagaagcagaaggggtgtgtgtgtgtgtgt 720
Db 917 cagttgtgctaatcatatgtgtgtaaaagaagaagcagaaggggtgtgtgtgtgtgtgt 976
QY 721 tctgtcctctccagcggaagaagacagagcagaaggtgagggcacaagtcattgagggcc 780
Db 977 tctgtcctctccagcggaagaagacagagcagaaggtgagggcacaagtcattgagggcc 1036
QY 781 tgcagagccctccgagcgtcaaccagctgagcggtgagagagagacaataaccctcacc 840
Db 1037 tgcagagccctccgagcgtcaaccagctgagcggtgagagagagacaataaccctcacc 1096
QY 841 gtagagagcccaaacactgacccacagactctgaccccca 881
Db 1097 gtagagagcccaaacactgacccacagactctgaccccca 1137

RESULT 4
T51737
ID T51737 standard; cDNA: 1724 BP.
AC T51737;
XX
XX 07-MAY-1997 (first entry)
DE Human herpes simplex virus cellular mediator cDNA.
XX
XX Herpes simplex virus cellular mediator; HVEM; receptor; HSV;
KW diagnosis; therapy; antisense; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 294..1145

```

```

FT FT sig_peptide /*tag= a
FT FT mat_peptide /*tag= b
FT FT /tag= c
FT FT /note= "the mature protein coding sequence is
FT FT preferred for use in constructs of the
FT FT invention"
PN W09704658-A1.
XX
XX 13-FEB-1997.
XX
XX 26-JUL-1996; 96WO-US12374.
XX
XX 28-JUL-1995; 95US-0509024.
XX
XX (NOUN ) UNITV NORTHWESTERN.
XX
XX Montgomery RI, Spear PG;
XX
XX MPI: 1997-145273/13.
XX
XX P-PSDB; W12659.
XX
XX New human herpes simplex virus cellular mediator - used for
XX diagnosis, drug screening and therapeutically to inhibit entry of
XX HSV into cells
XX
XX Claim 4; Page 37-38; 54pp; English.
XX
XX A cDNA insert (T51737) in plasmid pBEC580 codes for human herpes
XX simplex virus (HSV) cellular mediator (HVEM) (W12659), a novel
XX member of the TNF/NGF receptor family that mediates or enhances
XX entry of HSV into cells. It was isolated by screening a HeLa cDNA
XX expression library for genes capable of converting CHO-K1 cells
XX from resistance to susceptibility to HSV-1 entry. The clone can be
XX used to produce recombinant HVEM in host (esp. CHO) cells. Sense
XX oligonucleotides based on the sequence can be used as probes or
XX primers for identifying related sequences, while antisense
XX sequences can be used therapeutically to prevent HSV entry into
XX cells.
XX
XX Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 other;
SQ
Query Match 99.1%; Score 873; DB 18; Length 1724;
Best Local Similarity 99.4%; Pred. No. 1.8e-212;
Matches 876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 cctgagacatgagcctcctctgagactgggggctctcctctgagatcacccacagaa 60
Db 286 cctgagacatgagcctcctctgagactgggggctctcctctgagatcacccacagaa 345
QY 61 ccagactctgagagctgtgtgtatctcaacctctctggagagccctgtcagcccg 120
Db 346 ccagactctgagagctgtgtgtatctcaacctctctggagagccctgtcagcccg 405
QY 121 ctctgcctctctgcaagagagcctgtatctcaacctctctggagagccctgtcagcccg 180
Db 406 ctctgcctctctgcaagagagcctgtatctcaacctctctggagagccctgtcagcccg 465
QY 181 gtccaggtatctgtgtaagagagcctgagggagctgacgggacagatgtgtgaacct 240
Db 466 gtccaggtatctgtgtaagagagcctgagggagctgacgggacagatgtgtgaacct 525
QY 241 gccctccagacactatctgcccacactcaatgacctgaagcaagtgtctgcaatgcca 300
Db 526 gccctccagacactatctgcccacactcaatgacctgaagcaagtgtctgcaatgcca 585
QY 301 tctgtgtaaccagacatgtggctctgagcgagagccggaactgtctccagagacagcg 360
Db 586 tctgtgtaaccagacatgtggctctgagcgagagccggaactgtctccagagacagcg 645

```


QY 361 tgtgtgttgagcccaagccactctgtcatctgtccaaagagggagccactgcccgcgt 420
 Db 646 tgtgtgttgagcccaagccactctgtcatctgtccaaagagggagccactgcccgcgt 705
 QY 421 gccggtctaacgcccaccccgccgaggggtgcagaagaagagccagagc 480
 Db 706 gccggtctaacgcccaccccgccgaggggtgcagaagaagagccagagc 765
 QY 481 aggaacacctgtgtcagaactgtccccggggagactctctcccaatlggagccctggag 540
 Db 766 aggaacacctgtgtcagaactgtccccggggagactctctcccaatlggagccctggag 825
 QY 541 aatgtcaagaccagaccagcaagtgtcagctgtgtgagcaagagccggagcttgagca 600
 Db 826 aatgtcaagaccagaccagcaagtgtcagctgtgtgagcaagagccggagcttgagca 885
 QY 601 gctccactgtgtatgtgtgtctctcagaggagccctgtcatctgttctgtccca 660
 Db 886 gctccactgtgtatgtgtgtctctcagaggagccctgtcatctgttctgtccca 945
 QY 661 cagttgtcctaataatgtgtgaaagaagaccaggggtgatatgataagatga 720
 Db 946 cagttgtcctaataatgtgtgaaagaagaccaggggtgatatgataagatga 1005
 QY 721 tctgtctcgtccagcggaagaagacagagagagagagtgagagccagcttgagagcc 780
 Db 1006 tctgtctcgtccagcggaagaagacagagagagagagtgagagccagcttgagagcc 1065
 QY 781 tgcagggccctccgagctcaccacggtgtgcccgtggaggaacaatccctcattacgg 840
 Db 1066 tgcagggccctccgagctcaccacggtgtgcccgtggaggaacaatccctcattacgg 1125
 QY 841 ggaagagcccaaacactgtacccacagagctgtgaccccgca 881
 Db 1126 ggaagagcccaaacactgtacccacagagctgtgaccccgca 1166
 RESULT 5
 X25512
 ID X25512 standard; cDNA. 1724 BP.
 AC X25512;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE Herpes virus entry mediator (HVEM) cDNA.
 XX
 KW Herpes virus entry mediator; HVEM; HSV receptor; infection;
 KW diagnosis; therapy; vaccine; antiviral; assay; ds.
 XX
 OS Human herpes simplex virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 294..1145
 FT /*tag= a
 PN MO9920761-A2.
 PD 29-APR-1999.
 XX
 PF 22-OCT-1998; 98WO-US22342.
 XX
 PR 22-OCT-1997; 97US-0955531.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;
 XX
 DR WPI: 1999-302740/25.
 DR P-PSDB; Y05797.
 XX
 PT Human herpes simplex virus receptor B5 and HVEM compositions
 XX

PS Claim 12; Page 70-71; 89pp; English.
 XX
 CC This is the nucleotide sequence of HVEM (see Y05797), a novel
 CC human herpes simplex virus (HSV) entry mediator that is a member
 CC of the tumour necrosis factor receptor family. HVEM cDNA was
 CC isolated from a HeLa cell cDNA library on the basis of its
 CC ability to transfer HSV susceptibility to CHO cells. In the
 CC present invention, the combination of a novel porcine cell model
 CC system which is refractory to HCV entry, along with specific HSV
 CC B5 (see Y05796) and/or HVEM receptor proteins enables the
 CC development of assays for screening antiviral compounds and
 CC therapeutics. The assays are useful for detecting the ability of
 CC agents to inhibit HSV entry or spread and provide for facile
 CC high-throughput screening of compounds suspected to be able to
 CC inhibit such entry, e.g. compound libraries, peptide libraries
 CC etc., to identify potential drug candidates. The invention also
 CC provides a vaccine comprising the HSV receptor, an immunogenic
 CC polypeptide or fragments of the polypeptide.
 XX
 SQ Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 other;
 Query Match 99.1%; Score 873; DB 20; Length 1724;
 Best Local Similarity 99.4%; Pred. No. 1,8e-212;
 Matches 876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ccttaagcatgagagccctccttggaactgggggacctctcccttgagatccaccaccagaa 60
 Db 286 ccttaagcatgagagccctccttggaactgggggacctctcccttgagatccaccaccagaa 345
 QY 61 ccgagctcttgagctgtgtctgtatctcaactctctggagagccctgtctacgcccag 120
 Db 346 ccgagctcttgagctgtgtctgtatctcaactctctggagagccctgtctacgcccag 405
 QY 121 ctctgcgcgtctctgaagaagagagagtaaccagtggtctcagtggtgtgtcccaagtgca 180
 Db 406 ctctgcgcgtctctgaagaagagagtaaccagtggtctcagtggtgtgtcccaagtgca 465
 QY 181 gtccaggtatctgttgaagaagagccctgcgggagctgcagcgagcgacagtggtgaacct 240
 Db 466 gtccaggtatctgttgaagaagagccctgcgggagctgcagcgagcgacagtggtgaacct 525
 QY 241 gccctcagagaccataatgtccacactcaatgtcctaagaagaagtgtctgacgtgcca 300
 Db 526 gccctcagagaccataatgtccacactcaatgtcctaagaagaagtgtctgacgtgcca 585
 QY 301 tgtgtgaccagccatgtggtcctgcgcgagccggagactgtctccagagacagagccgcg 360
 Db 586 tgtgtgaccagccatgtggtcctgcgcgagccggagactgtctccagagacagagccgcg 645
 QY 361 tgtgtgttgagcccaagccactctgtcatctgtccaaagagggagccactgcccgcgt 420
 Db 646 tgtgtgttgagcccaagccactctgtcatctgtccaaagagggagccactgcccgcgt 705
 QY 421 gccggtctaacgcccaccccgccgaggggtgcagaagaagagccagagc 480
 Db 706 gccggtctaacgcccaccccgccgaggggtgcagaagaagagccagagc 765
 QY 481 aggaacacctgtgtcagaactgtccccggggagactctctcccaatlggagccctggag 540
 Db 766 aggaacacctgtgtcagaactgtccccggggagactctctcccaatlggagccctggag 825
 QY 541 aatgtcaagaccagaccagcaagtgtcagctgtgtgagcaagagccggagcttgagca 600
 Db 826 aatgtcaagaccagaccagcaagtgtcagctgtgtgagcaagagccggagcttgagca 885
 QY 601 gctccactgtgtatgtgtgtctctcagaggagccctgtcatctgttctgtccca 660
 Db 886 gctccactgtgtatgtgtgtctctcagaggagccctgtcatctgttctgtccca 945
 QY 661 cagttgtcctaataatgtgtgaaagaagaccaggggtgatatgataagatga 720
 Db 946 cagttgtcctaataatgtgtgaaagaagaccaggggtgatatgataagatga 1005

QY 721 tcgtctccgtccagcggaagacagagcgagagtgagccacagtcattgagccc 780
 CC |
 CC |
 CC |
 Db 1006 tcgtctccgtccagcggaagacagagcgagagtgagccacagtcattgagccc 1065
 CC |
 CC |
 CC |
 QY 781 tgaagcgcctcccgagcgtccacacagtgccgttgagagagacaatccatccacg 840
 CC |
 CC |
 CC |
 Db 1066 tgaagcgcctcccgagcgtccacacagtgccgttgagagagacaatccatccacg 1125
 CC |
 CC |
 CC |
 QY 841 ggaagagcccaaacacactgaaccacagactctgcaccccgga 881
 CC |
 CC |
 CC |
 Db 1126 ggaagagcccaaacacactgaaccacagactctgcaccccgga 1166
 CC |
 CC |
 CC |
 RESULT 6
 V44852
 ID V44852 standard; DNA: 927 BP.
 XX
 AC V44852;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Herpesvirus entry mediator gene.
 XX
 XX Entry mediator gene; herpesvirus; HVM; tumour necrosis factor receptor;
 KM gene expression regulator; cellular stress; inflammatory response;
 KM lymphocyte activity regulator; autoimmune response; ds.
 XX
 OS Herpesvirus.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 76..927
 FT /tag= a
 FT /product= HVM
 XX
 W09825967-A1.
 PN 18-JUN-1998.
 PD
 XX
 PF 05-DEC-1997; 97MO-US22278.
 XX
 PR 12-DEC-1996; 96US-0032705.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Marsters SA;
 XX
 DR WPI; 1998-348457/30.
 DR P-PSDB; W69238.
 XX
 PT Herpesvirus entry mediator polypeptide, HVM - useful, e.g. in
 PT assays for HVM and to produce antibodies and transgenic animals,
 PT e.g. for drug screening
 XX
 XX Example 1; Fig 1; 46pp; English.
 PS
 XX
 CC This sequence encodes the herpesvirus entry mediator (HVM) protein of
 CC the invention. The protein is useful in quantitative diagnostic assays
 CC for HVM. In affinity purification of HVM from recombinant cells/natural
 CC sources and in competitive-type receptor binding assays. It can also be
 CC used to generate antibodies, also useful in diagnostic assays for HVM
 CC and affinity purification of HVM. HVM is believed to be a member of the
 CC tumour necrosis factor receptor (TNFR) family, and transient transfection
 CC of HVM into human 293 cells caused marked activation of certain
 CC transcription factors, e.g. Ap-1, suggesting that HVM is involved in
 CC regulating gene expression in response to infectious stimuli and cellular
 CC stress. The predominant expression of HVM mRNA in lymphocyte-rich
 CC tissues (e.g. spleen and peripheral blood) also suggested it may be a
 CC receptor in regulating lymphocyte activity. Antibodies produced may be
 CC therefore be useful therapeutically, e.g. antagonistic antibodies may be
 CC useful to block excessive inflammatory/autoimmune response resulting from
 CC e.g. Ap-1 induction, whilst agonistic antibodies may enhance HVM
 CC regulation of such induction. The DNA may be used diagnostically, e.g.

CC to determine if DNA and/or RNA encoding HVM is present in cells, and to
 CC prepare HVM polypeptide recombinantly. It is also useful to produce
 CC non-human transgenic animals (e.g. mice or rats), especially knockout
 CC animals containing cells with an altered gene encoding HVM polypeptide.
 CC Such animals are useful in the development and screening of
 CC therapeutically useful reagents.

XX Sequence 927 BP; 185 A; 286 C; 291 G; 165 T; 0 other;

Query Match 97.4%; Score 856.4; DB 19; Length 927;
 Best Local Similarity 99.9%; Pred. No. 7.6e-209;
 Matches 859; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgaagcattgagagctcctccgtgagactgggggctctccctccctgagatccaccccgaga 60
 Db 68 cctgaagcattgagagctcctccgtgagactgggggctctccctccctgagatccaccccgaga 127
 QY 61 ccgagctctgagcgtgctgtatctatccactctcctggagcccccgtctacgcccag 120
 Db 128 ccgagctctgagcgtgctgtatctatccactctcctggagcccccgtctacgcccag 187
 QY 121 cctgcgcctctgcaagagagacagatccacagtggtgtccgagtgctgtcccaagtga 180
 Db 188 cctgcgcctctgcaagagagacagatccacagtggtgtccgagtgctgtcccaagtga 247
 QY 181 gtccaggtatcgtgtgaagagagcctctggggagctgcgggacagagtgctgaacct 240
 Db 248 gtccaggtatcgtgtgaagagagcctctggggagctgcgggacagagtgctgaacct 307
 QY 241 gccctccagacactcaatctgcccacactcaatctgccaatgaagcaatgtctcagtgccaa 300
 Db 308 gccctccagacactcaatctgcccacactcaatctgccaatgaagcaatgtctcagtgccaa 367
 QY 301 tgtgtaccacagcctatggtgctgcgagcgcgagacactgctccagagacagaaacgcg 360
 Db 368 tgtgtaccacagcctatggtgctgcgagcgcgagacactgctccagagacagaaacgcg 427
 QY 361 tgtgtgtgtagcagccagacactctctgcatctccagagacgagacactgctgcgcgt 420
 Db 428 tgtgtgtgtagcagccagacactctctgcatctccagagacgagacactgctgcgcgt 487
 QY 421 gccgcgttagcagccactccagcccgagcgaggtgtcagaagagagacacgagaatc 480
 Db 488 gccgcgttagcagccactccagcccgagcgaggtgtcagaagagagacacgagaatc 547
 QY 481 aggaacacctgtgtcagaatgtcccccggggagccttctcccaatgagaccttgag 540
 Db 548 aggaacacctgtgtcagaatgtcccccggggagccttctcccaatgagaccttgag 607
 QY 541 aatgtacagcacagacaaatgtagcgtgtgtgtgacgaagagcgagactgtaggacagca 600
 Db 608 aatgtacagcacagacaaatgtagcgtgtgtgtgacgaagagcgagactgtaggacagca 667
 QY 601 gtcctcactgtgtgtgttctctcagggagcctctcactcgtcatgttctgttctca 660
 Db 668 gtcctcactgtgtgtgttctctcagggagcctctcactcgtcatgttctgttctca 727
 QY 661 cagtgtgctatcatatgtgtgtaaaagaagaagcgaaggggtgtgtcagtcaagtga 720
 Db 728 cagtgtgctatcatatgtgtgtaaaagaagaagcgaaggggtgtgtcagtcaagtga 787
 QY 721 tcgtctccgtccagcggaagacagagcgagagtgtagccacagtcattgagccc 780
 Db 788 tcgtctccgtccagcggaagacagagcgagagtgtagccacagtcattgagccc 847
 QY 781 tgaagcgcctcccgagcgtccacacagtgccgttgagagagacaatccatccatccag 840
 Db 848 tgaagcgcctcccgagcgtccacacagtgccgttgagagagacaatccatccatccag 907
 QY 841 ggaagagcccaaacacactga 860
 Db 908 ggaagagcccaaacacactga 927

FH Key Location/Qualifiers
 FT CDS 103..936
 FT /tag= a
 FT /note= "this coding region is separately claimed
 FT in Claim 2"
 FT sig_peptide 103..206
 FT /tag= b
 FT mat_peptide 207..933
 FT /tag= c
 XX
 XX WO200014230-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 03-SEP-1999; 99WO-US20180.
 XX
 XX 03-SEP-1998; 98US-0146950.
 XX 29-JUN-1999; 99US-0342767.
 XX
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 XX Busfield SJ;
 XX
 XX WPI; 2000-256981/22.
 DR P-PSDB; Y79207.
 DR
 PT New nucleic acid molecule encoding herpes virus entry mediator (HVM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -
 XX
 XX Claim 2; Fig 7; 149pp; English.
 PS
 XX
 CC This full-length DNA sequence, the coding region of which is also
 CC claimed, corresponds to cDNA encoding human membrane-bound
 CC herpesvirus entry mediator-2 (mhVEM2, see Y79207), a novel form of
 CC membrane-bound herpesvirus entry mediator (mHVM). mHVM2 is a
 CC TANGO-69-receptor and member of the tumour necrosis factor receptor
 CC (TNFR) superfamily. The mHVM2 cDNA, deposited as ATCC 207171,
 CC was identified in a human mixed lymphocyte reaction library. HVM
 CC mediates the entry of herpes simplex virus (HSV) into cells. The
 CC invention is based on the discovery of 3 cDNA molecules (see
 CC 294195-97) which encode soluble forms (see Y79204-06) of mHVM, and
 CC on the present cDNA encoding mHVM2. In addition to isolated
 CC full-length proteins and polynucleotides, and invention provides
 CC TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor
 CC gene has been introduced or disrupted. DNA encoding HVM, HVM
 CC proteins and HVM antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVM proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVM
 CC agonists can be used to treat disorders associated with decreased
 CC HVM activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVM activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.
 CC
 XX Sequence 1834 BP; 398 A; 556 C; 539 G; 341 T; 0 other;
 XX
 XX
 Query Match 83.1%; Score 732.4; DB 21; Length 1834;
 Best Local Similarity 99.9%; Pred. No. 8.4e-177;
 Matches 733; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 ccttcgctctcgaaggaagacagtaaccagtgaggctccagatgctgccccaagtga 180
 DB 215 ccttcgctctcgaaggaagacagtaaccagtgaggctccagatgctgccccaagtga 274
 QY 181 gtccaggtatcgtgtgaaggaagcctgcgaggagctgtacagggacacagtgtgtgaacct 240
 DB 275 gtccaggtatcgtgtgaaggaagcctgcgaggagctgtacagggacacagtgtgtgaacct 334
 QY 241 ggcctcagagcactacattggccacctcaatagtgaagcaagtgtgtgaagtgaacaa 300
 DB 335 ggcctcagagcactacattggccacctcaatagtgaagcaagtgtgtgaagtgaacaa 394
 QY 301 tgtgtgaccagacatgagcctgcgagccgagcagactgtctccagagacagaagacgcg 360
 DB 395 tgtgtgaccagacatgagcctgcgagccgagcagactgtctccagagacagaagacgcg 454
 QY 361 tgtgtgtgtgacagccagagcacttctgcatcgttcaagagacggagacacatgcgcgagt 420
 DB 455 tgtgtgtgtgacagccagagcacttctgcatcgttcaagagacggagacacatgcgcgagt 514
 QY 421 ggcgcgttacggccacttcagcccgagcagaggtgtcagaagagagagacagagagtc 480
 DB 515 ggcgcgttacggccacttcagcccgagcagaggtgtcagaagagagagacagagagtc 574
 QY 481 aggaacacctgtgtcagaactgtcccccggagaccttctcccaatggagaccttgagg 540
 DB 575 aggaacacctgtgtcagaactgtcccccggagaccttctcccaatggagaccttgagg 634
 QY 541 aatgtcagcacacagacaaagtgtcagctgtgtgtgaagagcgcgagctgtgagcacaga 600
 DB 635 aatgtcagcacacagacaaagtgtcagctgtgtgtgaagagcgcgagctgtgagcacaga 694
 QY 601 gctcccaactgtgtgtgtgtgttctctcagaggagcctgtcatcgtcatgtgtgttcca 660
 DB 695 gctcccaactgtgtgtgtgtgttctctcagaggagcctgtcatcgtcatgtgtgttcca 754
 QY 661 cagttggcccaatcatatgtgtgaagaagaagacaaagggtgtgtgtatgtcaagttga 720
 DB 755 cagttggcccaatcatatgtgtgaagaagaagacaaagggtgtgtgtatgtcaagttga 814
 QY 721 tcgcttcgcgtccag 734
 DB 815 tcgcttcgcgtccag 828
 DB
 RESULT 9
 ID 294195
 XX 294195 standard; cDNA; 1929 BP.
 AC 294195;
 XX
 XX 19-JUN-2000 (first entry)
 DT
 XX
 XX Soluble herpesvirus entry mediator-1 (SHVEM1) cDNA.
 DE
 XX SHVEM-1: soluble herpesvirus entry mediator-1; TANGO-69-receptor;
 KW tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 297..878
 FT /tag= a
 FT /note= "this coding region is separately claimed
 FT in Claim 2"
 FT sig_peptide 297..404
 FT /tag= b
 FT mat_peptide 405..875
 FT /tag= c
 XX

XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 107..700
CDS /*tag= a
FT /note= "this coding region is separately claimed
FT sig-peptide 107..220
FT /*tag= b
FT mat-peptide 221..697
FT /*tag= c
XX WO200014230-A1.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99WO-US20180.
XX
XX 03-SEP-1998; 98US-0146950.
XX 29-JUN-1999; 99US-0342767.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Busfield SJ:
XX
XX WPI: 2000-256981/22.
XX P-PSDB; Y79205.
XX
XX New nucleic acid molecule encoding herpes virus entry mediator (HVM),
PT either in the soluble or membrane bound form, is useful in screening
PT assays and detection assays -
XX
XX
XX Claim 2; Fig 3; 149pp; English.
XX
XX This full-length DNA sequence, the coding region of which is also
CC claimed, corresponds to cDNA encoding human soluble herpesvirus
CC entry mediator-2 (SHVEM2, see Y79205), a novel soluble form of
CC membrane-bound herpesvirus entry mediator (mHVM). SHVEM2 is a
CC TANGO-69-receptor and member of the tumour necrosis factor receptor
CC (TNFR) superfamily. The SHVEM2 cDNA, deposited as ATCC 207173, was
CC identified in a human aortic endothelial cell cDNA library. SHVEM2
CC is thought to play a role analogous to other soluble members of the
CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
CC and lymphotoxin to bind mHVM, and to play a role in herpes simplex
CC virus (HSV) entry. The invention is based on the discovery of 3
CC cDNA molecules (see Z94195-97) which encode soluble forms (see
CC Y79204-06), and 1 cDNA molecule (see Z94198) that encodes a 2nd
CC membrane-bound form (see Y79207), of mHVM. In addition to
CC isolated full-length proteins and polynucleotides, and invention
CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
CC antibodies. Also provided are recombinant expression vectors,
CC host cells and transgenic animals in which a TANGO-69-receptor
CC gene has been introduced or disrupted. DNA encoding HVM, HVM
CC proteins and HVM antibodies can be used in screening and detection
CC assays (e.g. chromosomal mapping, tissue typing). HVM proteins
CC can also be used for regulation of cell proliferation, cell
CC differentiation, cell survival, inflammation mast cell activity,
CC HSV infection and/or proliferation, and/or coagulation. HVM
CC agonists can be used to treat disorders associated with decreased
CC HVM activity, e.g. proliferative disorders such as carcinoma or
CC pathogenic infection. Antagonists can be used to treat disorders
CC associated with increased HVM activity, e.g. autoimmune, T cell,
CC inflammatory and allergic inflammation disorders.
XX
XX Sequence 1596 BP; 341 A; 485 C; 483 G; 287 T; 0 other;
SQ

Query Match 76.28; Score 671.4; DB 21; Length 1596;
Best Local Similarity 84.98; Pred. No. 2.4e-161;
Matches 780; Conservative 0; Mismatches 101; Indels 38; Gaps 1;
QY 1 cctgagcatgagcctctctgagactggtggcctcctccctgagatccacccccagaa 60

Db 99 cctgagcatgagcctcctctgagactggtggcctcctccctgagatccacccccagaa 158
QY 61 ccgagccttgagcctctgctctgctatctccctcctcctggagagccccctgtacgccccag 120
Db 159 ccgagccttgagcctctgctctgctatctccctcctcctggagagccccctgtacgccccag 218
QY 121 cctgcgcctcctgcaagagagacagatccacagtggtgctcgcagtgctgccccagtca 180
Db 219 cctgcgcctcctgcaagagagacagatccacagtggtgctcgcagtgctgccccagtca 278
QY 181 gtcgaagttatcgttgaaagagagcctgcgggagagctgcagggcagatgtgtgaacct 240
Db 279 gtcgaagttatcgttgaaagagagcctgcgggagagctgcagggcagatgtgtgaacct 338
QY 241 gccctcagagcactatattgcccactcctaatggtcctcaagcaagtgtctcagtgccaaa 300
Db 339 gccctcagagcactatattgcccactcctaatggtcctcaagcaagtgtctcagtgccaaa 388
QY 301 tgtgtgacccagccatgagcctgcgcgcgagccggaactgtcctcagagacagaaacgcg 360
Db 399 tgtgtgacccagccatgagcctgcgcgcgagccggaactgtcctcagagacagaaacgcg 458
QY 361 tgtgtgctgcaagccagccactctgcacgtgcacagacggggagaccactgcgcgct 420
Db 459 tgtgtgctgcaagccagccactctgcacgtgcacagacggggagaccactgcgcgct 518
QY 421 gccgcgttacgcacactccaccccgagcagaggtggtcagaagggagggagccagagctc 480
Db 519 gccgcgttacgcacactccaccccgagcagaggtggtcagaagggagggagccagagctc 578
QY 481 agagacccctgtgtcagaactgtcccccggggagacctctcctccaaatggagacctgag 540
Db 579 agagacccctgtgtcagaactgtcccccggggagacctctcctccaaatggagacctgag 638
QY 541 aatgtacgacacagaccaaagt----- 562
Db 639 aatgtacgacacagaccaaattgtgcctaatcatatgtgtgaagaagaagccaaaggt 698
QY 563 cagctgctgtgtcagaagcccgagctgtgagccagacagctccacaggtatgtgtgt 622
Db 699 gagacacagcggcccatcagaaggtcatgtccacagcgtcacctcttgagctgttc 758
QY 623 tctctcagagagcctcctcctcgtcatgtgtgtgtccacagcttgccctaatatgtgt 682
Db 759 accccaagccttgagaggtgtgcccagagctttccagatcccggtgtccctccagggca 818
QY 683 gaaagaagaagaccaaagggtgattgattcaagtgatcgtctcgtccagcggaaaag 742
Db 819 gccactgcagcctgtggcaggtgattgattcaagtgatcgtctcgtccagcggaaaag 878
QY 743 acaggaagcagaaggtgagccacagatcattgagcctcctcagcctccgagctcac 802
Db 879 acaggaagcagaaggtgagccacagatcattgagcctcctcagcctccgagctcac 938
QY 803 caccgttcgctgtgagagacaaatattccatccacggggagagacccaaacactgacc 862
Db 939 caccgttcgctgtgagagacaaatattccatccacggggagagacccaaacactgacc 998
QY 863 cacaagactgcaccccca 881
Db 999 cacagactgcaccccca 1017
RESULT 11
Z94197
ID Z94197 standard; cDNA; 2313 BP.
XX
XX AC Z94197;
XX
XX DT 19-JUN-2000 (first entry)
XX Soluble herpesvirus entry mediator-3 (SHVEM3) cDNA.

XX SHVEM-3; soluble herpesvirus entry mediator-3; TANGO-69-receptor;
 KW tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

85..645

/*tag= a

FT sig_peptide 85..198 /note= "this coding region is separately claimed

/*tag= b

199..642

mat_peptide /tag= c

XX WO200014230-A1.

16-MAR-2000.

03-SEP-1999; 99MO-US20180.

03-SEP-1998; 98US-0146950.

29-JUN-1999; 99US-0342767.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Busfield SJ;

WPI: 2000-256981/22.

P-PSDB; Y79206.

XX New nucleic acid molecule encoding herpes virus entry mediator (HYEM),

either in the soluble or membrane bound form, is useful in screening

assays and detection assays -

Claim 2; Fig 5; 149pp: English.

XX This full-length DNA sequence, the coding region of which is also

claimed, corresponds to cDNA encoding human soluble herpesvirus

entry mediator-3 (SHVEM3, see Y79206), a novel soluble form of

membrane-bound herpesvirus entry mediator (mHYEM). SHVEM3 is a

TANGO-69-receptor and member of the tumour necrosis factor receptor

XX (TNFR) superfamily. The SHVEM3 cDNA, deposited as AFCC 207172, was

identified in a human mixed lymphocyte reaction library. SHVEM3

is thought to play a role analogous to other soluble members of the

TNFR superfamily by interfering with the ability of LIGHT-TANGO-69

and lymphotoxin to bind mHYEM, and to play a role in herpes simplex

XX virus (HSV) entry. The invention is based on the discovery of 3

cDNA molecules (see 294195-97) which encode soluble forms (see

Y79204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd

membrane-bound form (see Y79207), of mHYEM. In addition to

isolated full-length proteins and polynucleotides, and invention

XX provides TANGO-69-receptor fusion proteins, antigenic peptides and

antibodies. Also provided are recombinant expression vectors,

host cells and transgenic animals in which a TANGO-69-receptor

gene has been introduced or disrupted. DNA encoding HYEM, HYEM

proteins and HYEM antibodies can be used in screening and detection

XX assays (e.g. chromosomal mapping, tissue typing). HYEM proteins

can also be used for regulation of cell proliferation, cell

differentiation, cell survival, inflammation mast cell activity,

HSV infection and/or proliferation, and/or coagulation. HYEM

agonists can be used to treat disorders associated with decreased

XX HYEM activity, e.g. proliferative disorders such as carcinoma or

pathogenic infection. Antagonists can be used to treat disorders

associated with increased HYEM activity, e.g. autoimmune, T cell,

inflammatory and allergic inflammation disorders.

Sequence 2313 BP; 411 A; 762 C; 689 G; 451 T; 0 other;

Query Match 63.18; Score 555.8; DB 21; Length 2313;
 Best Local Similarity 99.6%; Pred. No. 5.6e-132;
 Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctgagcatggaagccctccctggaagactgggggctccctccctgtagatccaccccgaa 60

DB 77 cctgagcatggaagccctccctggaagactgggggctccctccctgtagatccaccccgaa 136

QY 61 ccgacgcttgagcgtgtgtgtatctcaacctccctccggagccctctgtaagcccg 120

DB 137 ccgacgcttgagcgtgtgtgtatctcaacctccctccggagccctctgtaagcccg 196

QY 121 cctcgcctccctgcaagagagacgagaccagtggtgctcgaatgtgtgcccagtca 180

DB 197 cctcgcctccctgcaagagagacgagaccagtggtgctcgaatgtgtgcccagtca 256

QY 181 gtcaggtatctgtgtaagagagcctcgtggggagcctgcaagggagacagtgtgaaacct 240

DB 257 gtcaggtatctgtgtaagagagcctcgtggggagcctgcaagggagacagtgtgaaacct 316

QY 241 gccctcaggaacctatctgcccacctcaatgagccttaagcaagtgtctcagtgccaaa 300

DB 317 gccctcaggaacctatctgcccacctcaatgagccttaagcaagtgtctcagtgccaaa 376

QY 301 tgtgtgacccagcattggtgctgctgagccgagacgtgtccaggaacagagacgcg 360

DB 377 tgtgtgacccagcattggtgctgctgagccgagacgtgtccaggaacagagacgcg 436

QY 361 tgtgtgtgtcagccagccagcctctgcatctgtccagagacggagacactgtgcgcgt 420

DB 437 tgtgtgtgtcagccagccagcctctgcatctgtccagagacggagacactgtgcgcgt 486

QY 421 gccgccttaagccacctccagcccgagccagagagtggtcagaagggagcaccagagtc 480

DB 497 gccgccttaagccacctccagcccgagccagagagtggtcagaagggagcaccagagtc 556

QY 481 aggaacacctgtgtcagaactgccccggggagacctctctccaatgtgacctgtgag 540

DB 557 aggaacacctgtgtcagaactgccccggggagacctctctccaatgtgacctgtgag 616

QY 541 aatgtacagcaccagcaaa 559

DB 617 aatgtacagcaccagcaaa 635

RESULT 12

V34510 V34510 standard; cDNA; 2692 BP.

XX AC V34510;

XX DT 25-SEP-1998 (first entry)

XX DE Human TNF receptor related splice variant 1 (TR2-SV1) gene.

XX KW de: human; tumour necrosis factor; TNF; herpes simplex virus;

KW aberrant cell survival; radiation therapy; lymphocyte proliferation;

KW immune deficiency syndrome.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 373..930

FT sig_peptide /tag= a /product= "TR2 protein"

FT mat_peptide /tag= b /tag= c

XX WO9818824-A1.

XX PD 07-MAY-1998.

CC can be used as reagents for detecting/measuring soluble forms of
CC protein in the circulation.
XX
SQ Sequence 723 BP; 140 A; 222 C; 225 G; 136 T; 0 other;

Query Match 34.8%; Score 306.2; DB 17; Length 723;
Best Local Similarity 99.0%; Pred. No. 8.5e-69;
Matches 308; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 atgagagctctgagagctgggggctccctccctggagatccaccaccagaacagcgtc 68
DB 1 atgagagctccctgagagctgggggctccctccctggagatccaccaccagaacagcgtc 60
QY 69 ttgagagctgtgtctgtatccacactctctggagagccctctgtaagcccaagctgtcgc 128
DB 61 ttgagagctgtgtctgtatccacactctctggagagccctctgtaagcccaagctgtcgc 120
QY 129 tctgtcaagagagagagatcccaagtgagctccagtgctgtcccaagtgcaagtcaggt 188
DB 121 tctgtcaagagagagagatcccaagtgagctccagtgctgtcccaagtgcaagtcaggt 180
QY 189 tatcgtgtgaagagagagctctggggagctgagcgagcgacagtgtgtgaacctgtcccca 248
DB 181 tatcgtgtgaagagagagctctggggagctgagcgagcgacagtgtgtgaacctgtcccca 240
QY 249 ggcacacacattggccacccaatgagcctaagcaagtgctgtcagtgccaatgtgtgac 308
DB 241 ggcacacacattggccacccaatgagcctaagcaagtgctgtcagtgccaatgtgtgac 300
QY 309 ccagagcattggg 319
DB 301 ccagatattgg 311

RESULT 14
V34511
ID V34511 standard; cDNA; 2637 BP.

XX V34511;
AC
XX
DT 25-SEP-1998 (first entry)
XX
DE Human TNF receptor related splice variant 2 (TR2-SV2) gene.
XX
XX ds: human: tumour necrosis factor; TNF; herpes simplex virus;
KM aberrant cell survival; radiation therapy; lymphocyte proliferation;
XX immune deficiency syndrome.
XX
XX Homo sapiens.

XX OS
FH Key Location/Qualifiers
FT CDS 247..657
FT /tag= a
FT /product= "TR2 protein"

XX MO9818824-A1.
XX
XX PD 07-MAY-1998.
XX
XX PF 30-OCT-1996; 96MO-US18540.
XX
XX PR 30-OCT-1996; 96MO-US18540.
XX
XX

XX (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Gentz RL, Hurle MR, Lyn SDP, Ni J, Rosen CA;
XX
XX WPI: 1998-272139/24.
XX DR P-PSDB; W60047.
XX
XX

PT Nucleic acid encoding TR2 tumour necrosis factor family receptor -

PT and its splice variants, useful for diagnosis and treatment of
PT diseases involving abnormal cell survival or death, e.g. herpes
PT simplex infection
XX
XX

XX Claim 2; p95-96; 151pp; English.

XX The human tumour necrosis factor (TNF) receptor related protein (TR2) is
CC a member of the TNF family and displays considerable homology to murine
CC CD40. It can be used in soluble forms to treat herpes simplex virus
CC infection and TR2 proteins (or their agonists or antagonists) are used to
CC treat disease associated with aberrant cell survival. Agonists may also
CC be used to protect against the effects of radiation therapy and to
CC stimulate lymphocyte proliferation and differentiation in patients
CC infected by human immune deficiency syndrome.
XX
XX

SQ Sequence 2637 BP; 454 A; 881 C; 776 G; 526 T; 0 other;

Query Match 27.2%; Score 239.4; DB 19; Length 2637;
Best Local Similarity 99.2%; Pred. No. 1.1e-51;
Matches 251; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 309 ccagcattgggctgtgcgagagccggaactgtctccagacagaagacgcgtgtgtgt 368
DB 400 ccagcattgggctgtgcgagagccggaactgtctccagacagaagacgcgtgtgtgtgt 459
QY 369 ttgagccagagcactctgtcatcgtccagagcgaggaacacgtgcgcgtgtccgcgt 428
DB 460 ttgagccagagcactctgtcatcgtccagagcgaggaacacgtgcgcgtgtccgcgt 519
QY 429 taagcaccctccagcccgagcgaggtgtcagaagggagcaccgagtgtagaacacc 488
DB 520 taagcaccctccagcccgagcgaggtgtcagaagggagcaccgagtgtagaacacc 579
QY 489 ctgtgtcagaactgcgcccccgggagacctctctcccaatggagacctgtgaggaatgtcag 548
DB 580 ctgtgtcagaactgcgcccccgggagacctctctcccaatggagacctgtgaggaatgtcag 638
QY 549 caccagaccaggt 561
DB 639 caccagaccaggt 651

RESULT 15
T40050

ID T40050 standard; cDNA; 405 BP.

XX T40050;
AC
XX
XX

DT 30-JUN-1997 (first entry)
XX
XX

DE Human tumour necrosis factor receptor splice variant 2 cDNA.

XX Human: tumour necrosis factor; TNF; receptor; treatment;
XX activation; inhibition; identification; agonist; antagonist;
XX stimulation; T cell; differentiation; mediation; immune;
XX antiviral; response; regulation; growth; protection; HIV;
XX radiation; Chlamydia; infection; immunodeficiency; virus;
XX autoimmune disease; inflammation; septic shock; cerebral; malaria;
XX cachexia; B cell; cancer; graft; host; reaction; rejection;
XX prevention; apoptosis; cytotoxicity; hybridisation probe;
XX detection; antibody; reagent; splice variant 2; SV2; ss.
XX
XX

XX Homo sapiens.

XX OS
FH Key Location/Qualifiers
FT CDS 1..405
FT /tag= a
FT /product= tumour_necrosis_factor_SV2

XX MO9634095-A1.
XX
XX

XX 31-OCT-1996.
XX
XX

XX 27-APR-1995; 95WO-US05058.
 PF
 XX
 PR 27-APR-1995; 95WO-US05058.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz R, Ni J, Rosen CA;
 XX
 DR WPI; 1996-497627/49.
 DR P-PSDB; W05811.
 XX
 PT New nucleic acid encoding a human tumour necrosis factor receptor -
 PT useful for treatment of auto-immune diseases etc., in diagnosis and
 PT for drug screening
 XX
 XX
 PS Claim 14; Page 49; 73pp; English.
 CC
 CC The present sequence encodes the human tumour necrosis factor (TNF)
 CC receptor splice variant 2 (SV2), which may be used for the
 CC identification of TNF SV2 receptor agonists or antagonists. TNF SV2
 CC receptor agonists inhibit tumour growth, stimulate cell (e.g.
 CC T cell) differentiation, mediate the immune and antiviral
 CC responses, regulate growth, protect against radiation and Chlamydia
 CC infection, and can be used to treat immunodeficiencies, e.g. human
 CC immunodeficiency virus. Antagonists can be used to treat T cell
 CC mediated autoimmune disease, inflammation, septic shock, cerebral
 CC malaria, cachexia or B cell cancers, to inhibit graft-host
 CC reactions and to prevent apoptosis or cytotoxicity. Fragments of
 CC the TNF SV2 receptor encoding DNA can be used as hybridisation
 CC probes for detecting related genes. Antibodies against the protein
 CC can be used as reagents for detecting/measuring soluble forms of
 CC protein in the circulation.
 XX
 SQ Sequence 405 BP; 68 A; 140 C; 127 G; 70 T; 0 other;

Query Match 26.5%; Score 233.4; DB 17; Length 405;
 Best Local Similarity 93.7%; Pred. No. 2.1e-50;
 Matches 254; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
 QY 291 caatgccaatgtgtgaccagccatgagcgtgagcgagccggaactgtccagaca 350
 Db 130 cagccctctctctgtgactcagcatgctgcgagccggaactgtccagaca 189
 QY 351 gagaacgcgtgtgtgtgagccagccactctgtcatgltccagagcgagaccac 410
 Db 190 gagaacgcgtgtgtgtgagccagccactctgtcatgltccagagcgagaccac 249
 QY 411 tggcgcgcgtgagccgactcagccgcgggccaagaggtgacagaaggagac 470
 Db 250 tggcgcgcgtgagccgactcagccgcgggccaagaggtgacagaaggagac 309
 QY 471 accgagagtcagacaccctgtgtcagaactgcccccgaggacacttctcccaatgag 530
 Db 310 accgagagtcagacaccctgtgtcagaactgcccccgaggacacttctcccaatgag 368
 QY 531 accctggaggaatgtcagcacagaccagaagt 561
 Db 369 accctggaggaatgtcagcacagaccagaagt 399

Search completed: April 24, 2001, 18:40:14
 Job time: 16052 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 16:55:20 ; Search time 1458.62 Seconds
(without alignments)
8279.381 Million cell updates/sec

Title: US-08-741-095b-25
Perfect score: 881
Sequence: 1 cctgagagctgagagctcctc.....ccacagactctgcaccccca 881

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 6853842396 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_om:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
8: gb_pr1:*
9: gb_pr2:*
10: gb_pr3:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: em_fun:*
15: em_hum1:*
16: em_hum2:*
17: em_in:*
18: em_om:*
19: em_or:*
20: em_ov:*
21: em_pat:*
22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_sts:*
26: em_sy:*
27: em_un:*
28: em_vl:*
29: gb_htg1:*
30: gb_htg2:*
31: gb_in1:*
32: gb_in2:*
33: em_ba1:*
34: em_ba2:*
35: em_hum3:*
36: em_hum4:*
37: gb_pr4:*
38: gb_htg3:*
39: gb_htg4:*
40: gb_htg5:*
41: gb_htg6:*
42: gb_htg7:*
43: em_htg1:*

44: em_htg2:*
45: em_htg3:*
46: em_hum5:*
47: gb_pl3:*
48: gb_pr5:*
49: gb_htg8:*
50: gb_htg9:*
51: gb_htg10:*
52: gb_htg11:*
53: gb_htg12:*
54: gb_htg13:*
55: gb_htg14:*
56: gb_in3:*
57: gb_htg15:*
58: gb_htg16:*
59: gb_htg17:*
60: em_htg4:*
61: em_htg5:*
62: em_htg6:*
63: em_htg7:*
64: em_hum6:*
65: gb_htg18:*
66: gb_htg19:*
67: gb_htg20:*
68: gb_htg21:*
69: gb_htg22:*
70: gb_htg23:*
71: gb_vil:*
72: gb_vil2:*
73: gb_ba3:*
74: em_htg8:*
75: em_htg9:*
76: em_htg10:*
77: gb_pr6:*
78: gb_pr7:*
79: gb_sts1:*
80: gb_sts2:*
81: gb_pat1:*
82: gb_pat2:*
83: em_htg90:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879.4	99.8	1681	37	AF153978 Homo sapi
2	879.4	99.8	1704	13	AX022023 Sequence
3	879.4	99.8	1704	78	HSU81232 Human tumor
4	879.4	99.8	1724	78	HSU70321 Human herpe
5	869	78.2	852	37	AF147720 Chloroce
6	342.2	38.8	2692	13	AX022026 Sequence
7	239.4	27.2	2637	13	AX022029 Sequence
8	160.6	18.2	154530	66	AL139246 Homo sapi
9	89	10.1	154530	66	AL139246 Homo sapi
10	76.4	8.7	837	3	AX027018 Sequence
11	76.4	8.7	845	3	AX027450 Sequence
12	60.8	6.9	2136	85	HUMTNRFP L04270 Homo sapien
13	60.8	6.9	2148	37	AK027080 Homo sapi
14	60.4	6.9	2394	85	HUMTNRFP M55994 Human tumor
15	59.6	6.8	691	81	I36350 Sequence 12
16	58	6.6	1557	81	I36197 Sequence 3
17	58	6.6	1641	81	I36196 Sequence 1
18	58	6.6	2253	81	A78517 Sequence 1
19	58	6.6	3380	79	G26865 human STS S
20	58	6.6	3492	85	S63368 tumor necro
21	58	6.6	3683	85	M32315 Human tumor

22	57	6.5	834	48	AX027007	Sequence
23	57	6.5	1004	78	HSCDW40	X60592 Human CD40
24	57	6.5	1004	81	I07284	X01284 Sequence 31
25	55.8	6.3	519	81	AR076920	Sequence
26	55.8	6.3	519	81	AR078310	Sequence
27	55.8	6.3	519	81	AR085413	Sequence
28	55.4	6.3	807	3	AX027021	Sequence
29	55.4	6.3	815	3	BTU57745	U57745 Bos taurus
30	53.8	6.1	1614	11	MUSLYMPHOB	L38423 Mus musculus
31	53.8	6.1	2076	11	MMU29173	U29173 Mus musculus
32	52.6	6.0	870	11	AX027014	Sequence
33	52.6	6.0	1579	11	MUSCD40A	M8312 Mouse CD40
34	49.4	5.6	5820	71	AF145588	Stealth v
35	48.6	5.5	1017	11	RSOX40	X17037 Rat mRNA fo
36	47.8	5.4	4181	8	AB029021	Homo sapi
37	47.8	5.4	174253	57	AC068590	Homo sapi
38	47.4	5.4	157634	55	AC060233	Homo sapi
39	47.4	5.4	180188	40	AC015656	Homo sapi
40	47.4	5.4	187966	9	AC006487	Homo sapi
41	47.2	5.4	1600	81	A43530	Sequence 1
42	47.2	5.4	3386	85	HUMNGFR	M14764 Human nerve
43	46.4	5.3	2339	81	A26415	CDNA fragme
44	46.2	5.2	1505	11	MUSMTFR2	M60465 Mouse tumor
45	46.2	5.2	3796	11	MUSTNFR1	M59378 Murine tumor

ALIGNMENTS

RESULT 1
LOCUS AF153978 1681 bp mRNA PRI 13-JUN-2000
DEFINITION Homo sapiens CD40-like protein precursor mRNA, complete cds.
ACCESSION AF153978
VERSION AF153978.1 GI:8489096

KEYWORDS

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1681)
Zhang, W., Wan, T. and Cao, X.
Direct Submission
Submitted (25-MAY-1999) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Road, Shanghai 200433, P.R. China
Location/Qualifiers

FEATURES

source

1..1681
/organism="Homo sapiens"
/db_xref="taxon:9606"
246..1097
/codon_start=1
/product="CD40-like protein precursor"
/protein_id="AAF73588.1"
/db_xref="GI:8489097"
/translation="MEPPDGMGPPPMRSTPKTDVLRVLYFLGAPCYAPALPSCKE
DEYVSECCPKSPGKYRKAEGLTGVCPGPTVIAHLNGLSKLOCOMCDPA
MGLRASRNSCTRENAVCGSGPHCIYODGHCACRAATASPGORVOKGTESODT
LCQNPPTGTFSPNGTLECCQHOTKCSMLVTKAGAGTSSHHWMLSGSLVIVCST
VGLICVKKRRKPRGDVYKIVSVQRRKDEAEATVIEALQAPPVTVIVAVETLPSF
TGRSPNH"

CDS

BASE COUNT 336 a 520 c 499 g 326 t
ORIGIN

Query Match 99.8%; Score 879.4; DB 37; Length 1681;
Best Local Similarity 99.9%; Pred. No. 6.7e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cctgaagcattgagcctctcctgagactggggcctcctcctggaatcacaccacagaa 60
|||||
DB 238 CCTGAGCATTGAGCCTCTCTGAGACTGGGGGCTCTCTCCCTGAGATCACCCCAAAA 297

OY	61	cctgaagcattgagcctctcctgagactggggcctcctcctggaatcacaccacagaa 120
DB	298	CCGACGCTCTTGAAGGCTGGTGTATCTATCTCCTCTGGAGGCCCTCTACGGCCAG 357
OY	121	ctctgcctcctcgaag 180
DB	358	CTCTGCGCTCTCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417
OY	181	gtcccaagttatctgtgtgaagagagagagagagagagagagagagagagagagag 240
DB	418	GTCACAGTTATCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477
OY	241	gacctcagagcactcatttgcacactcactcactcactcactcactcactcactcact 300
DB	478	GCCCTCAGGACCTTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCC 537
OY	301	tgtgtgaccagcattgagcctcctcctcctcctcctcctcctcctcctcctcctcct 360
DB	538	TGTGTGACCCAGCCATGGGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
OY	361	tgtgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
DB	598	TGTGTGTTGCAAGCCAGGCTTCTGATGATGATGATGATGATGATGATGATGATGAT 657
OY	421	gcccgccttaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
DB	658	GCCGCGCTTACGCTACCTTCAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 717
OY	481	aggaacacctgtgtgaagactgcccccgaggagagagagagagagagagagagagag 540
DB	718	AGCACACCTGTGTGAGAACTGCCCCCGGGAGCTTCTCTCCAAATGGAGACCTGGA 777
OY	541	aattgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
DB	778	AATGTAGACACAGACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
OY	601	gtcccaactgt 660
DB	838	GCTCCACAGTGGATGT 897
OY	661	caattgacctatcatatgt 720
DB	898	CAGTTGGCTTAATCATATGTGTGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 957
OY	721	tgtgtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
DB	958	TGCTCTCGTCCAGCGGAGAAAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1017
OY	781	tgaagcagcctcctcgaagcagcagcagcagcagcagcagcagcagcagcagcagcag 840
DB	1018	TGCAGGCGCCCTCCGAGCGTCCACACAGCGTGCCTGTGAGAGACAATATCCCTATTC 1077
OY	841	ggaag 881
DB	1078	GGAGGAGGCCCAACACACAGCTGACACAGACTGTGACCCCGA 1118
RESULT 2		
LOCUS	AX022023	1704 bp DNA
DEFINITION	Sequence 1 from Patent EP0961782.	UNA
ACCESSION	AX022023	
VERSION	AX022023.1	GI:10045729
KEYWORDS		
SOURCE	unidentified.	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 1704)	
AUTHORS	Hurle, M.R., Lyn, S.D., Ni, J., Rosen, C.A. and Gentz, R.L.	
TITLE	Human tumor necrosis factor receptor-like 2	
JOURNAL	Patent: EP 0961782-A 08-DEC-1999;	
FEATURES	HUMAN GENOME SCIENCES INC (US); SMITHKLINE BEECHAM CORP (US)	
	Location/Qualifiers	

source 1. 1704
/organism="unidentified"
/db_xref="taxon:32644"
sig_peptide 265..372
CDS 265..1116
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC07836.1"
/db_xref="GI:10045730"
/translation="MEPPDMDGPPWRSPKTDVLRVLYLFLGAPCYAPALPSCKE
DEYVSGECPCSPGYRKYKACGLTGVCEPGRVYIAHLNGLSKLOCOMDPA
MGLRASRNCSTRENAVCCSGPGRFCTVODGDHACACRAVATSSPGOROKGTESODT
LCQNCPPGTFSPNGTLEECQHOTKCSMLVTRAGACTSSHWMLSSGLVIVYVST
VGLICVRRKRRPRGDVAVIVSVORRKEABEAEVIALQAPDVTVAVEETIPSE
TGRSPNH"

mat_peptide 373..1113
BASE COUNT 343 a 529 c 504 g 328 t
ORIGIN

Query Match 99.8%; Score 879.4; DB 13; Length 1704;
Best Local Similarity 99.9%; Pred. No. 6.7e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgagcattgagcctcctctgagactggggcctccctctgagatccacccacagaa 60
DB 257 CCGAGGCAATGAGAGCTCCCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCAAAA 316

QY 61 ccgagcttctgagcctggtgtatctacacctctgagagccctctgaccccg 120
DB 317 CCGACGCTTGAGGCTGTGCTATCTACCTCTGGAGGCCCCCTGTCAGGCCAG 376

QY 121 cctctgcctctcaaggaagacagataccagttgagctcagagttctgcccagtgca 180
DB 377 CTCTGCCCTCTCAAGAGAGAGAGATACCAATGGGCTCCGAGTGTGCCCAAGTGCA 436

QY 181 gtccaggtatcgtgtgaagagcctgcyggagctgacgagggcacaagtgtgtgaacct 240
DB 437 GTCCAGGTTATCGTGTGAAGAGAGGCTGCGGGAGCTGAGCGGACACAGTGTGAACCT 496

QY 241 ggcctcagcactactatctgcccactcaatgtcctaagcaagtgtctgcaatgcca 300
DB 497 GCCCTCCAGGACCTACATGTCGCCACCTCAATGGCTTAACAGATCTCTCAAGTGC 556

QY 301 tctgtacccagcattgagcctgcyggagcagcagcagcagcagcagcagcagcagc 360
DB 557 TGTGTACCCAGGACATGGGCTGCGGCGAGCGGAATCTCTCAGAGACAGAAACGCC 616

QY 361 tctgtgtgtgagcagcagcagcacttctgacgtcagagaaggggaaccatgcygcg 420
DB 617 TGTGTGTGTGCAAGCCAGGCACTTCTGCTCAGAGAGCGGGGACCACTGCGCGCG 676

QY 421 ggcgagcttaagcagcactcagcagcagcagcagcagcagcagcagcagcagcagc 480
DB 677 GCGGCGCTTACGACCTCCAGCCGCGGAGAGGTGCAAGAGGAGGACCGAAGATC 736

QY 481 aggaacacctgtgtcagaactgcccccgaggacacttctcccaatggagacccctgag 540
DB 737 AGGACACCTGTGTGCAAGACTGCCCGGGGACCTTCTCTCCATGGGACCTTGAGG 796

QY 541 aatgtacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 600
DB 797 AATGTACAGCAGCAGCAAGTGTGAGCTGTGCTGACGAAGGCGGAGCTGGGACAGCA 856

QY 601 gctcccaactggtatgtgttctctcagagagcctctcactgcacattgtttgtca 660
DB 857 GCTCCCACTGGGATGTGTCTCTCAAGGAGCTTCGTCATGTCATTTGTTGTCCA 916

QY 661 caatttgacctaatcatatgtgtgaagaagaagaagcagaggtgtgtgaagcagtgca 720
DB 917 CAATTGGCCATATCATATGTGTGAAGAAGAAGCAAGGGGTGTATGTATGAAGTGA 976

QY 721 tctgtctcgttcagcaggaagacagagcagaggtgagccacagtcattgagccc 780

DB 977 TCGTCTCCGCTCAGCGGAAAAAGACAGAGAGCAGAAAGTGTAGGCGCACATGATGAGGCC 1036

QY 781 tgcagagccctcccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 840

DB 1037 TGCAGGCCCCCTCCGAGAGCTACACACGCTGCGCTGGAGAGACAAATACCTCATTCACGG 1096

QY 841 ggaagagcccaaacactgaccacacagactctgaccccg 881

DB 1097 GGAGAGCCCAACCACTGACCCAGACTCTGACCCCGA 1137

RESULT 3
HSU81232
LOCUS HSU81232 1704 bp mRNA PRI 05-JAN-1999
DEFINITION Human tumor necrosis factor receptor-like gene 2 (TR2) mRNA,
complete cds.
ACCESSION U81232
VERSION U81232.1 GI:4098958
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Kwon,B.S., Tan,K.B. and Ni,J.
TITLE A newly-identified member of the tumor necrosis factor receptor
superfamily with a wide tissue distribution and involvement in
lymphocyte activation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1704)
AUTHORS Ni,J.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1996) Protein Expression and Purification, Human
Genome Sciences, Inc., 9410 Key West Ave., Rockville, MD
20850-3338, USA

FEATURES
source
Location/Qualifiers
1..1704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.2-36.3"
1..1704
/gene="TR2"
265..1116
/gene="TR2"
/codon_start=1
/product="tumor necrosis factor receptor-like gene 2"
/protein_id="AAD00505.1"
/db_xref="GI:4098959"

QY 1 cctgagcattgagcctcctctgagactggggcctccctctgagatccacccacagaa 60
DB 257 CCGAGGCAATGAGAGCTCCCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCAAAA 316

QY 61 ccgagcttctgagcctggtgtatctacacctctgagagccctctgaccccg 120
DB 317 CCGACGCTTGAGGCTGTGCTATCTACCTCTGGAGGCCCCCTGTCAGGCCAG 376

QY 121 cctctgcctctcaaggaagacagagcagaggtgagccacagtcattgagccc 180

Query Match 99.8%; Score 879.4; DB 78; Length 1704;
Best Local Similarity 99.9%; Pred. No. 6.7e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cctgagcattgagcctcctctgagactggggcctccctctgagatccacccacagaa 60
DB 257 CCGAGGCAATGAGAGCTCCCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCAAAA 316

QY 61 ccgagcttctgagcctggtgtatctacacctctgagagccctctgaccccg 120
DB 317 CCGACGCTTGAGGCTGTGCTATCTACCTCTGGAGGCCCCCTGTCAGGCCAG 376

QY 121 cctctgcctctcaaggaagacagagcagaggtgagccacagtcattgagccc 180

```

|||||
Db 377 CTCTGCCGCTCTCCAGAGAGAGAGACTACCCAGTGGGCTCCGATGCTGCCCAAGTGA 436
QY 181 gtccaggtatctgtgaaagaagcctgcggagagctgaaaggacagtggtgtgaacct 240
Db 437 GTCCAGGTTATCTGTGAAGAGAGGCGCTGCGGAGCTGAGCGGACAGTGTGTGAACCT 496
QY 241 gccctcagacactacatctgcccacactcaatggcctaagaagtgtctgcaatgcca 300
Db 497 GCCCTCCAGGACTTACATTTGCCACTCTCAATGGCCCTAAGCAAGTGTCTCAGTGGCAA 556
QY 301 tgttgaccagcaatgagcctgcggcgagaccggaactgtctcagagacagaaacgcg 360
Db 557 TGTGTGACCCAGGACATGAGGCGCTGCGGCGAGCGGAACCTCTCAGAGACAGAACGCCG 616
QY 361 tgtgtgttgcaaccccaagagcactcttgcactgtctcagagacagggagacactgcgcgt 420
Db 617 TGTGTGTGTCACACCCAGGCGCTTGTGATGTCCAGAGAGGAGACCACTGCGCCGCT 676
QY 421 gccgcgttacgcacactcaccagcccgagagaggtgtcagaagaagagagaccagagtc 480
Db 677 GCCGCGTTACGCGACTCTCCAGCCCGGCGCAGAGGTTGCAAGAGAGGACCGAGAGTC 736
QY 481 aggacacccctgtgtcagaactgcccccgaggagacctctctcccaatgagacccctgag 540
Db 737 AGGACACCTGTGTGAGAACTGCCCGCGGAGACTTCTCTCCAAATGGAGACCTGGAGG 796
QY 541 aatgtacagcccaagcaaatgtcagctggtgtgtgaaagaagccggagcctggagaccga 600
Db 797 AATGTGAGCACCGACCAAGTGTGAGCTGTGTGAGAGAGGCGGAGCTGTGAGACCGCA 856
QY 601 gccccaactggtatggtgttctctcagagagccctgcacatgcatgtgtgtgtccca 660
Db 857 GCTCCCACTGTGTGATGTGTGTTCTCTCAAGGAGCCTCGTCAATGTGTGTGTGTCTCA 916
QY 661 caattggcctaatacatatgtgtgaaagaagaagcaaggggtgtatgtatgtaagtga 720
Db 917 CAGTTGGCTTAATCATATGTGTGTAAGAAAGAAAGCAAGGGGTGATGTGTGTAAGTGA 976
QY 721 tctgttcctgtcagcggaagaagaagagagagagagagagagagagagagagagag 780
Db 977 TCTGTCTCCGTCCAGCGGAAAGACAGAGAGCAAGAGTGAAGGCGCACAGTCAATTGAGGCC 1036
QY 781 tgaagagccctcgcagagctaacacagtggtgcgtgtgagagagacataaccttcaacg 840
Db 1037 TGAAGGCGCTCCGGAGCTACCAAGGTGCGCTGTGAGAGAGACAATTCCTCAATTCAGG 1096
QY 841 ggaagagcccaaacactgacacagagactgtcaccccgga 881
Db 1097 GGAGAGACCCAAACCACTGACCAAGACTCTGCACCCCGA 1137

RESULT 4
LOCUS HS070321 1724 bp mRNA PRI 31-MAY-1997
DEFINITION Human herpesvirus entry mediator mRNA, complete cds.
ACCESSION U70321
VERSION U70321.1 GI:2138189
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1724)
AUTHORS Montgomery,R.I., Warner,M.S., Lum,B.J. and Spear,P.G.
TITLE Herpes simplex virus-1 entry into cells mediated by a novel member
of the TNF/NGF receptor family
JOURNAL Cell 87 (3), 427-436 (1996)
MEDLINE 97053782
REFERENCE
2 (bases 1 to 1724)
AUTHORS Montgomery,R.I., Warner,M.S., Lum,B. and Spear,P.G.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-1996) Micro-Immuno, W213, Northwestern Univ., 303

```

```

COMMENT E. Chicago Ave, Chicago, IL 60611, USA
On May 31, 1997 this sequence version replaced gi:1657771.
FEATURES
source
CDS
E. Chicago Ave, Chicago, IL 60611, USA
Location/Qualifiers
1..1724
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
294..1145
/feature="HEM: member of TNF/NGF receptor family"
/product="herpesvirus entry mediator"
/protein_id="AAB58354.1"
/db_xref="GI:2138190"
/translation="MEPPDMDPPPMRSTPRTDVLRLVLYTLFLGAPCAPALPSCKE
DEYVSECCPKSPGYRYKACGELTGVCPGPGYIAHLNLSKLCLOMCPDA
MGLRSRNSRREBNVACGSPGPFCTVDDGDMCAKRYATSPGPROROKGTESOT
LCQCPGPFSPNGTLEQHOTKCSMLTKAGACTSSHHWMLFSLSLVLYVCS
VGLICVNRKRPRGDVAVIVSVORRKEAEATVIRALQAPDVTVAVEETIPSF
TGRSPNH"
BASE COUNT 331 a 548 c 512 g 333 t
ORIGIN
Query Match 99.8%; Score 879.4; DB 78; Length 1724;
Best Local Similarity 99.9%; Pred. No. 6,6e-181;
Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 cctgaagcatgagagcctctcgtgagagctgaggcctctccctgagagatccaccccaaga 60
Db 286 CCTGAGGACATGAGGCGCTCTCGAGAGCTGGGGGCTCTCTCTGAGATCACCCTCCAGAA 345
QY 61 ccgaagcttctgaagcctggtgtgtatctcaacctctctgagagccctctgaagcccaag 120
Db 346 CCGAGCTTTGAGGCTGTGTGTATCTCACTTCTGGAGAGCCCTCTGACGCCCGAG 405
QY 121 ctctgcgtctcctcaagagagagagtaaccagtggtgtcagatgtgtgtcccaagtga 180
Db 406 CTCTGCCGCTCTCAAGAGAGAGAGAGTACCAAGTGGGCTCTCGAGTCTGCCCAAGTGA 465
QY 181 gtccaggtatctgtgaaagaagcctgcggagagagagagagagagagagagagagag 240
Db 466 GTCCAGGTTATCTGTGAAGAGAGGCGCTGCGGAGGTGAGCGGACAGTGTGAACCT 525
QY 241 gccctcagacactacatctgcccacactcaatgagcctaagaagaagtgtctcagatgcca 300
Db 526 GCCCTCCAGGACTTACATTTGCCACTCTCAATGGCCCTAAGCAAGTGTCTGCAATGCAAA 585
QY 301 tgttgaccagcaatgagcctgcggcgagccggaactgtctcagagacagaaacgcg 360
Db 586 TGTGTGACCCAGGACATGAGGCGCTGCGGCGAGCGGAACGTGTCCAGAGACAGAAACGCCG 645
QY 361 tgtgtgttgcaagcagagcactctgcatctgctcagagagagagagagagagagagag 420
Db 646 TGTGTGTGTCGACCCAGGCGCTTGTGATCTCCAGAGACGGGAGCCACTGCGCGCT 705
QY 421 gccgcgttacgcacactcaccagcccgagagagagagagagagagagagagagagag 480
Db 706 GCCGCGCTTACGCGACTCTCCAGCGGCGCAGAGGTGAGAGAGGAGCAGCAGAGTC 765
QY 481 aggacacccctgtgtcagaactgcccccgaggagacctctctcccaatgagacccctgag 540
Db 766 AGGACACCTGTGTGAGAACTGCCCGGAGACCTTCTCTCCAAATGGAGACCTGTGAGG 825
QY 541 aatgtacagcccaagcaaatgtcagctggtgtgtgaaagaagccggaagctggagaccga 600
Db 826 AATGTGAGCACCGACCAAGTGTGAGCTGTGTGAGAGAGGCGGAGCGGAGCGGAGACGCA 885
QY 601 gccccaactggtatggtgttctctcagagagagagagagagagagagagagagagag 660
Db 886 GCTCCCACTGTGTGATGTGTGTCTCTCAAGGAGCGCTGTCAATGTGTGTGTGTGTCTCA 945
QY 661 caattggcctaatacatatgtgtgaaagaagaagcaaggggtgtatgtatgtaagtga 720

```

Db 946 CAGTTGGCCTAATCATATGTGTGAAAAAGAAAGCCAGGGGTGATGTAGTCAAGGTGA 1005
 QY 721 tctcttcctccacagcggaaagacagagcagaaggttgagccacagatattgagggcc 780
 Db 1006 TCGTCTCCGTCCAGCGGAAAGAGAGGAGAGAGGTGAGGCCACAGTATTGAGGCC 1065
 QY 781 tgcagccctccgagagtlacacacaggttgccgltgagagagacaatcaccttccag 840
 Db 1066 TGGAGGCGCCCTCGGAGAGTCACACAGGTGCGGTGGAGGAGACATATCCCTCATTCACGG 1125
 QY 841 gtagagagcccaaacacactgacccacagactctgcacccga 881
 Db 1126 GGAAGAGCCCAACCACTGACCCACAGACTGTGACCCCGA 1166
 RESULT 5
 AF147720 852 bp mRNA PRI 13-JUL-1999
 LOCUS AF147720
 DEFINITION Chlocoebus aethiops Hveas (Hveas) complete.cds.
 ACCESSION AF147720
 VERSION AF147720.1 GI:5002247
 KEYWORDS
 SOURCE African green monkey.
 ORGANISM Cercopithecus aethiops
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 Cercopithecinae; Cercopithecus.
 REFERENCE 1 (bases 1 to 852)
 AUTHORS Foster, T.P., Choulienjo, V.N. and Kousoulas, K.G.
 TITLE Functional characterization of the Hvea homolog specified by
 JOURNAL African green monkey kidney cells with a herpes simplex virus
 MEDLINE expressing the green fluorescence protein
 PUBMED Virology 258 (2), 365-374 (1999)
 10365573
 REFERENCE 2 (bases 1 to 852)
 AUTHORS Foster, T.P., Choulienjo, V.N. and Kousoulas, K.G.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-1999) Veterinary Microbiology, Louisiana State
 University-School of Vet. Med., South Stadium Rd., Baton Rouge, LA
 70803, USA
 FEATURES
 source
 1. 852
 /location="Qualifiers"
 /organism="Cercopithecus aethiops"
 /db_xref="taxon:9534"
 /cell_type="vero"
 /tissue_type="kidney"
 1. 852
 /gene="Hveas"
 1. 852
 /gene="Hveas"
 /function="co-receptor that mediates entry of herpes
 simplex virus type 1"
 /note="similar to Homo sapiens Hvea"
 /codon_start=1
 /product="Hveas"
 /protein_id="AAD37381.1"
 /db_xref="GI:5002248"
 /translation="MEPPGSGSPRRAPKADILTLVLYTLFLSSCYAPLPSCKE
 DEYVSGECPCRCGPGFHVROACGEOTGVBCPSPGTYIAHNGLSKLOCOMCPA
 MGLRTSRNCSSTANALCGSPGHFCITODGDCACARAYATSPGQRYVKGSTESODT
 LCONCPGTFSSNGTLEECOHGKMSKMLVTGAGPQTSRRVWMLISGLIYIVG
 LILRLITGVKRKSRGVDYKIVSVQRKROAEGALIVTEAVQPPDITVAVERTE
 PAFTRGS"
 BASE COUNT 176 a 257 c 264 g 155 t
 ORIGIN
 Query Match 78.2% Score 689; DB 37; Length 852;
 Best Local Similarity 90.7% Pred. No. 1.5e-139;
 Matches 770; Conservative 0; Mismatches 70; Indels 9; Gaps 3;
 QY 9 atgagagctcttgagagcttgagggtctctcctgagatccaccccgagacgagctc 68

Db 1 ATGAGAGCTCTCTGAGAGTTGGGGGTCTCTCCCGGAGAGCCCGCCCAAGCGGACATC 60
 QY 69 ttagagctgtgtgtatctcaccttctcgtggagagcccccgtacgccccagctgtgcg 128
 Db 61 TTGACGCTGGTGTGTATCTCACCTTCTGTGGATCTCTGTTACGCGCCAGCTGTGCC 120
 QY 129 tctctgaag 188
 Db 121 TCTTGCAG 180
 QY 189 tctctgaag 248
 Db 181 TTTCACGCTGAG 240
 QY 249 ggcacttaacttgccaccccaatggccttaagagagagagagagagagagagagag 308
 Db 241 GGGAGCTTACATTTCTCATTTCAATGGCTGAGCAAGTGTGTGACAGTCCAAATGTGAC 300
 QY 309 ccagacatggcctgc 368
 Db 301 CAGACCATGGGCTGCGGCACAAACCGGAACTGCTCCACAGACAGAGAGAGAGAGAG 360
 QY 369 tgcagccagagccactctgcagctgcagagagagagagagagagagagagagagag 428
 Db 361 TGCAGGCCAGAGGCACATTTGATCATTCATTCAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 429 taagcactccagcccgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 488
 Db 421 TAGCCACCTCCAGCCCGCCGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 489 ctgtgcag 548
 Db 481 CTGTGTACAG 540
 QY 549 caccagacacagatgcagc---tgctgtgtgaagagagagagagagagagagagag 605
 Db 541 CACGGAGAACAGTGCAGAGCAATATGCTGTGACGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 606 cactgt 659
 Db 601 CGCTGGGT 660
 QY 660 acagcttgcccttaactatgtgtgaagagagagagagagagagagagagagagagag 719
 Db 661 ATACTTCCGCTATCATATGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 720 atcgtctcgttcagcggaaagacagagagagagagagagagagagagagagagag 779
 Db 721 ATCGTCTCCGTCAGCGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 780 ctgcagagccctccgag 839
 Db 781 GTGACAGGCCCTCCGAGATCACACAGGTGCGGTGAGAGAGAGAGAGAGAGAGAG 840
 QY 840 gtagagagc 848
 Db 841 GGGAGAGAGC 849
 RESULT 6
 AX022026 2692 bp DNA UNA 07-SEP-2000
 LOCUS AX022026
 DEFINITION Sequence 4 from Patent EP0961782.
 ACCESSION AX022026
 VERSION AX022026.1 GI:10045731
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2692)
 AUTHORS Hurle, M.R., Lyn, S.D., Ni, J., Rosen, C.A. and Gentz, R.L.
 TITLE Human tumor necrosis factor receptor-like 2


```

OY      369      tgcagccagggccactctcgtatcgtccaaagagggagccactcgcgcgtccgcgct 428
Db 138799      TGcAGCCcAGGcCAcTTcGTcATcGTcTcAGAcGcGGAcCAcAcTcTcGcGcGTcCcGcGT 138858
OY      429      tacgcacctccaaagccgggcccagaggtgcagagagggagagcaccagatcagagacc 488
Db 138859      TAGCCACAcTTCACcCGCGGcCAGAGGcGTGCAGAAgAGAGGTAAcGCGGTGcGTGCcGAGC 138918
OY      489      ctgtgtcagaactcgtcccccgaggacc 515
Db 138919      ACCcCTCCAcTTTCACcCGGTGcTCCc 138945

RESULT      9
ALI39246/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

ALI39246      154530 bp      DNA      HTG      10-AUG-2000
Homo sapiens chromosome 1 clone RP3-395M20 map p36.11-36.33, ***
SEQUENCING IN PROGRESS ***, 6 unordered pieces.
ALI39246
ALI39246.6      GI:9796372
HTG; HTGS_PHASE1; HTGS_DNAFLT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154530)
Plumb,B.
Direct Submission
Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humuery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 11, 2000 this sequence version replaced gi:9367391.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humuery@sanger.ac.uk
----- Project Information
Center project name: dj395M20
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 152602 bases at least Q40
Consensus quality: 153318 bases at least Q30
Consensus quality: 153701 bases at least Q20
Insert size: 154030; sum-of-ctrls
Insert size: 167102; 1.8% error; agarose-fp
Quality coverage: 6.88x in Q20 bases; sum-of-ctrls Quality
coverage: 6.34x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1      23698: contig of 23698 bp in length
*      23699      23798: gap of      100 bp
*      23799      46060: contig of 22262 bp in length
*      46061      46160: gap of      100 bp
*      46161      100189: contig of 54029 bp in length
*      100190      100289: gap of      100 bp
*      100290      108179: contig of 7890 bp in length
*      108180      108279: gap of      100 bp
*      108280      129035: contig of 20756 bp in length
*      129036      129136: gap of      100 bp
*      129136      154530: contig of 25395 bp in length.
*
* Location/Qualifiers
*
* 1.      154530

```

```

/misc_feature /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p36.11-36.33"
/clone="RP3-395M20"
/clone_lib="RPCI-3"
1..23698
/note="assembly_fragment:00746
fragment_chain:1"
misc_feature /note="assembly_fragment:00410
fragment_chain:1"
46161..100189
/note="assembly_fragment:00468
fragment_chain:1"
100290..108179
/note="assembly_fragment:02473
fragment_chain:2"
108280..129035
/note="assembly_fragment:02562
fragment_chain:2"
misc_feature /note="assembly_fragment:01243"
129136..154530
BASE COUNT 29475 a 48692 c 47274 g 28589 t 500 others
ORIGIN

```

Query Match 10.18; Score 89; DB 66; Length 154530;
 Best Local Similarity 75.98; Pred. No. 4.8e-10;
 Matches 110; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```

QY 562 gcagctgctgtgtaagagccgagctgtgaccagactccactgggtatgtcgt 621
||||| ||||||| ||||| ||||| ||||||| ||||| ||||| ||||| |||||
Db 144081 GCAGCTGCTGTGTAAGAGCCGAGCTGTGACCAGACTCCCGTGGTGTGATTC 144022

QY 622 ttctctcaaggagctgtcatcgttctgtccacagtgtgcttaatacatatgtg 681
|-| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -| -|
Db 144021 TCTCAGGAGCCTCATCTCATCATCTTCCTCACACTTGCCCTATCTCATGCA 143962

QY 682 tgaagaagaagaagcaagggtgtga 706
||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 143961 TGAAGAAGAAGAATCAAGGGTGA 143937

```

```

RESULT 10
LOCUS AX027018 837 bp DNA MAM 16-SEP-2000
DEFINITION Sequence 15 from Patent WO0037102.
ACCESSION AX027018
VERSION AX027018.1 GI:10188046
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 837)
Rogers,N.J., Dörfling,A. and Lechler,R.I.
Immunosuppression
Patent: WO 0037102-A 29-JUN-2000;
ROGERS NICHOLA JANE (GB) ; DÖRLING ANTHONY (GB) ; ML LAB PLC (GB) ;
LECHLER ROBERT IAN (GB)
FEATURES
source
1..837
location/Qualifiers
1..837
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 207 a 231 c 221 g 178 t
ORIGIN

```

Query Match 8.7%; Score 76.4; DB 3; Length 837;
 Best Local Similarity 51.08; Pred. No. 1e-06;
 Matches 213; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

```

QY 103 cccctctctacgccccagctctgcgtctctgcaaggagagtaaccagtgtgcgcg 162
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 CCGCGCTCCACACCAGAACCCACCACTTCATGCAAGAAACCATATCCACAAACAGCC 106

QY 163 agtgcgtcccaagtgcagtcaggatatactgttgaaggagcctcgggagctacgg 222
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 107 GGTGCTTAATTGTGTGCCCGCCAGAGACAGAACTGGTGAACCACTGCACAGAGTCACTG 166

QY 223 gacagtggtgaacctgtccctccagagcacctacattgtccaccccaatgagctaga 282
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 167 AACAGAAATGCTTCCTTGTGAGTTCCAGCAATTCCTAGCACTGGAAATAGAGAAC 226

QY 283 agtgcgtcagtgccaatgtgtgacccaacatgagcctgcgcgcgcgcgcgcgcgcgc 342
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 227 ACGTGATATGACCAATAATATGTGGACCCCACTAGGTCTCCAGGTCCAGAGGAGGCA 286

QY 343 ccaggaagaagaacgcgtgtgtgtgtgacccagagccacttcgtcatgtccaggaag 402
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 CCTCGAAMACAGACACCACTTGTGTGTGAGTAGAGGCCATCACTGTACCAACAGCGCCT 346

QY 403 gggaccactgcgcgcgtgtgcgcgtttagccacccctccagcccgagaggtgacaga 462
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 GTGAAGTTGCACCTTG-----CACAGCTTGTGCTTCCCTGGCTCGGGGTCAAGC 397

QY 463 agggagcaccgagagtcagagacaccctgtgtcagaactcccccgaggacctctc 520
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 AGATGGCGACAGAGGTTTCTGACATATCTGTGAACCCCTGCCAGTTGGCTTCTTC 455

```

```

RESULT 11
LOCUS AX027450 845 bp DNA MAM 16-SEP-2000
DEFINITION Sequence 3 from Patent WO0039294.
ACCESSION AX027450
VERSION AX027450.1 GI:10188416
KEYWORDS
SOURCE
ORGANISM
Sus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 845)
Bravery,C., Thompson,S. and Rushworth,S.
Porcine cells incapable of expressing cd40 antigen, for
xenotransplantation
Patent: WO 0039294-A 06-JUL-2000;
NOVARTIS ERIND VERNALT GMBH (AT) ; NOVARTIS AG (CH) ; BRAVERY
CHRISTOPHER (GB) ; THOMPSON SIMON (GB) ; RUSHWORTH STUART (GB)
JOURNAL
1..845
location/Qualifiers
1..845
/organism="Sus sp."
/db_xref="taxon:9826"
BASE COUNT 206 a 237 c 224 g 178 t
ORIGIN

```

Query Match 8.7%; Score 76.4; DB 3; Length 845;
 Best Local Similarity 51.08; Pred. No. 1e-06;
 Matches 213; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

```

QY 103 cccctctctacgccccagctctgcgtctctgcaaggagagtaaccagtgtgcgcg 162
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 55 CCGCGCTCCACACCAGAACCCACCACTTCATGCAAGAAACCAATACCAACAAACAGCC 114

QY 163 agtgcgtcccaagtgcagtcaggatatactgttgaaggagcctcgggagctacgg 222
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 115 GGTGCTTAATTGTGTGCCCGCCAGAGACAGAACTGGTGAACCACTGCACAGAGTCACTG 174

QY 223 gacagtggtgaacctgtccctccagagcacctacattgtccaccccaatgagctaga 282
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 AACAGAAATGCTTCCTTGTGAGTTCCAGCAATTCCTAGCACTGGAAATAGAGAAC 234

QY 283 agtgcgtcagtgccaatgtgtgacccaacatgagcctgcgcgcgcgcgcgcgcgcgc 342
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db	235	ACTGTCATCAGACAACTAATCTCGACACCACCACTTAGTCTCCAGGTCCAGAGGAGGGCA	294
OY	343	ccaaggacagagaagcgccgltgtlgttgcagcccagaccactctcgtcatcgtccagagc	402
Db	295	CTCGAAAAACAACACACACTTGTTGTGTGCAGGAAGGCCATCATCTAACACAGCGCT	354
OY	403	gggaccactggcgcggtgcgcgcttcagcgaacctccagccccgggccaagatgtgcaga	462
Db	355	GCGAAAGTTGCAACCTTG-----CACAGCTTGTGCTTCCCTGCGCTCGGGGTCAAGC	405
OY	463	agggaagcacccagtagtcaagacacacctgtgtcagaactgcccccggagacccttc	520
Db	406	AGATGGCAGACAGAGGTTTCTGACACTATCTGTGAACCCCTGCCAGTTGGCTTCTTC	463
RESULT	12		
HUMTNFRP			
LOCUS			
DEFINITION	HUMTNFRP	2136 bp	mRNA
			PRI 03-AUG-1993
			tumor necrosis factor receptor 2 related
ACCESSION			
VERSION	L04270.1	GI:339761	
KEYWORDS	tumor necrosis factor receptor 2 related protein.		
SOURCE	Homo sapiens (library: Liver cDNA of P.M.)		Liver cDNA to mRNA.
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	Baens,M., Chaffanel,M., Cassiman,J.J., Van den Berghe,H. and		
JOURNAL	Maynen,P.		
MEDLINE	Construction and evaluation of a hncDNA library of human 12p		
FEATURES	transcribed sequences derived from a somatic cell hybrid		
	Genomics 16, 214-218 (1993)		
	93252381		
source			
	Location/Qualifiers		
	1..2136		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/tissue_type="Liver"		
	/tissue_lib="Liver cDNA of P.M."		
	169..1476		
	/note="putative"		
	/codon_start=1		
	/product="tumor necrosis factor receptor 2 related		
	protein"		
	/protein_id="AAA36757.1"		
	/xref="GI:339762"		
	/translation="MLTPKMTSAFGLAMGPLVGLRFLIASAQPAVPVASENQTNR		
	DDEEVEYEPQHRTICSRCPPTVYSACSRIIDVVCATVCENSTNEHWNVITTDCLR		
	PCDVMGLEIAETAPCTSKTKQCRCOPMFCAMALKECHLELSDCPGEAEILKDEVL		
	GKGNNHCVPCKAGHFONTSSPSARCOPEHTENGLEYEAAGTAOSDTCKNPLEDE		
	PEMSGMTLMVLLPLAFILLPLLATVFCSIKMSHSPLSLKGRPOGPGPVAVG		
	SWMPKKAHYPFPDLVOPRLIPISGVDSVSYCIAPAYLEAKGVPOOQSPLDTERPOL		
	PGESOVVAHGNTGITHVTGSGMTITGNITYINGPVLGGPPGEGDI.PATIEPPPIPEER		
	DPCGPGGSTPHQDEGKMHMLEHEHCATNSRNGRPNOFTTHD"		
BASE COUNT	446 a	706 c	608 g
ORIGIN			376 t
Query Match	6.9%	Score 60.8,	DB 85; Length 2136;
Best Local Similarity	51.5%;	Pred. No. 0.0019;	
Matches 140:	Conservative 0;	Mismatches 132;	Indels 0; Gaps 0;
OY	135	aaggagacgcgttacccagtgtggtcgcgcagatgtgtcccccagaatgcagtcaggttatcgt	194
Db	310	AAGGAATCTTAGACGCCACCGACACCGCATCTGTCTGTCTCCCGCTGCCCGCAGGACCTAT	369
OY	195	gtgaagagagcctgtgcggggaaagctgacgggacaagtgltgaacctgtccctccaggaacc	254
Db	370	GTCCTACGATAATATGAGCCGATCCGGACACACAGTTTGTCCACATGTGCGAGAATTCC	429
OY	255	tacattgccacactcaatagcgcctaagaagtgltctgcagttgccaaaatgttgtaccagcc	314

Db	430	TACAAAGAGACTGGAACACTGACCAATCTGCGACACTGTGCCGCCCTGTGATCCAGTG	489
Qy	315	atgggcccgtcgcgagccggaactgctccagagacagaaacgcgtgtgtgtgcagc	374
Db	490	atggcccttcgagagagattgcccccttcgacacgaacggaagaccagtcgctccag	549
Qy	375	caaggccactcttcgcatcgctccagacgaggga	406
Db	550	CCGGGAATGTTCTGTGCTGCTGGGCCCTCGA	581
RESULT 13			
AK027080	2148	bp	mRNA
LOCUS	AK027080	2148	bp
DEFINITION	Homo sapiens CDNA: FLJ33427 fls, clone HRC04788, highly similar to HUNTNRFP Homo sapiens tumor necrosis factor receptor 2 related protein mRNA.		
VERSION	AK027080		
KEYWORDS	AK027080.1	GI:10440111	
SOURCE	Oligo capping: fls (full insert sequence). Homo sapiens primary human renal epithelial cells cDNA to mRNA, clone.lib:HRC clone:HRC04788.		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (sites) Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEBO human cDNA sequencing project Unpublished (2000) 2 (bases 1 to 2148) Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y. Direct Submission Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
TITLE	NEBO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).		
FEATURES	Location/Qualifiers 1..2148 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_type="primary human renal epithelial cells" /clone="HRC04788" /clone_lib="HRC" /note="Cloning vector pME18SFL3" 1..2148 /note="Highly similar to HUNTNRFP Homo sapiens tumor necrosis factor receptor 2 related protein mRNA"		
BASE COUNT	462 a	705 c	606 g
ORIGIN	375 t		
Query Match			
Best Local Similarity	51.5%	Score NO. 60.8:	DB 37; Length 2148;
Matches 140:	Conservative	0;	Mismatches 132; Indels 0; Gaps 0;
Qy	135	aagagagcagatccacgcagtggtgcgcagtgctgtccccaagtgcagtcaggtatcgt	194
Db	333	AAGGAATGACTATGAGCCCGACCGCATCTGCTCTCCCGCTGCCCGGACGACCTACT	392
Qy	195	gtgaagagagcctcgcggtgagagctgaagagcacagtgtgtgaacctgtccctccagcacc	254


```
OY 284 gfgtcgcaatgccaatgltgaccagccatgggctcgcgagccggaactgtc 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 348 GTGCTTGAGCTGTGG--CTCCCGCTGTAGCTTGACCGAGGTGGAACCTCAAGCCTGCAC 404
OY 344 cagagcagagagacgcgtgtgtgtgagccagagccactctgcatcgtccagagc 403
    || | |||| | ||| |||| | ||| | ||| | ||| |
Db 405 TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGTACTGTGGCGCTGAGCAAGCA 464
OY 404 ggaccactgagccggtgagcgtltaagccactccagcccgagccagaggtgcagaa 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 GGAGGGGTGCCGGCTGTGCGCGCGCTGCAGAGTGGCGCGGCTTCGGGTGGCCAG 524
OY 464 gggagagcagagagtcaggaacacctgtgcagaactgcccccgaggacctctcc 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 ACCAGGAACAGAAATCAGACGTGTGTGTGCAAGCCTGTGCCCGGGGACGTTCTCAA 584
OY 524 ca 525
    || ||
Db 585 CA 586
```

Search completed: April 24, 2001, 19:08:11
Job time: 7971 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 15:17:28 ; Search time 63.85 Seconds
(Without alignments)
2409.162 Million cell updates/sec

Title: US-08-741-095B-25
Perfect score: 881
Sequence: 1 cctgagcattgagcctcct.....ccacgactcgcaccgca 881

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq:*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
3: /cgnl_7/ptodata/1/ina/5A_COMB.seq:*
4: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfillsl.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.3	99.1	1724	5	PCT-US96-12374-1 Sequence 1, Appl
2	59.6	6.8	691	1	US-08-266-080B-12 Sequence 12, Appl
3	59.6	6.8	691	5	PCT-US95-05423-12 Sequence 12, Appl
4	58	6.6	1557	1	US-08-385-229-3 Sequence 3, Appl
5	58	6.6	1641	1	US-08-385-229-1 Sequence 1, Appl
6	58	6.6	1641	2	US-08-650-000-1 Sequence 1, Appl
7	58	6.6	1641	6	5395760-1 Patent No. 5395760
8	57	6.5	1004	4	US-09-071-433-85 Sequence 85, Appl
9	55.8	6.3	519	2	US-08-249-189-4 Sequence 4, Appl
10	55.8	6.3	519	2	US-08-484-624A-4 Sequence 4, Appl
11	55.8	6.3	519	3	US-08-477-733B-4 Sequence 4, Appl
12	55.8	6.3	519	3	US-09-088-913A-4 Sequence 4, Appl
13	47.2	5.4	1600	3	US-08-602-791-1 Sequence 1, Appl
14	46.2	5.2	3796	2	US-08-762-308-11 Sequence 11, Appl
15	46.2	5.2	3813	2	US-08-650-000-3 Sequence 3, Appl
16	46.2	5.2	3813	6	5395760-3 Patent No. 5395760
17	42.2	4.8	1006	4	US-08-911-423-3 Sequence 1, Appl
18	41.8	4.7	1788	1	US-08-225-989-1 Sequence 1, Appl
19	41.8	4.7	1788	1	US-08-570-923-1 Sequence 1, Appl
20	41.8	4.7	1788	1	US-08-580-014-1 Sequence 1, Appl
21	41.8	4.7	1788	4	US-09-079-785-1 Sequence 1, Appl
22	41.8	4.7	3627	2	US-08-232-087A-1 Sequence 1, Appl
23	41.4	4.7	848	1	US-08-192-480A-1 Sequence 1, Appl
24	39.2	4.4	1057	1	US-08-147-784-1 Sequence 1, Appl
25	38.8	4.4	618	1	US-08-097-827-6 Sequence 6, Appl
26	38.8	4.4	618	1	US-08-494-574-6 Sequence 6, Appl
27	38.8	4.4	1317	1	US-08-097-827-10 Sequence 10, Appl

28	38.8	4.4	1317	1	US-08-494-574-10	Sequence 10, Appl
29	38.4	4.4	1464	4	US-09-188-930-255	Sequence 255, Appl
30	38.4	4.4	1633	4	US-09-188-930-73	Sequence 73, Appl
31	37	4.2	1878	3	US-08-996-139-14	Sequence 14, Appl
32	36.4	4.1	759	4	US-09-042-785A-6	Sequence 6, Appl
33	36.4	4.1	1164	2	US-08-794-796-1	Sequence 1, Appl
34	36.4	4.1	1815	4	US-09-042-785A-24	Sequence 24, Appl
35	36.4	4.1	2186	3	US-08-959-382-1	Sequence 1, Appl
36	36.4	4.1	2612	4	US-09-042-785A-23	Sequence 23, Appl
37	36.4	4.1	2638	4	US-09-042-785A-22	Sequence 22, Appl
38	36.2	4.1	1391	3	US-08-896-139-3	Sequence 3, Appl
39	36.2	4.1	3115	3	US-08-896-139-1	Sequence 1, Appl
40	36.2	4.1	3136	3	US-08-996-139-5	Sequence 5, Appl
41	36.2	4.1	3136	4	US-09-435-296-3	Sequence 3, Appl
42	36	4.1	1719	4	US-09-042-785A-5	Sequence 5, Appl
43	36	4.1	3331	4	US-09-042-785A-1	Sequence 1, Appl
44	36	4.1	18318	1	US-08-414-926A-6	Sequence 6, Appl
45	36	4.1	18318	2	US-08-926-922-6	Sequence 6, Appl

ALIGNMENTS

```
RESULT 1
PCT-US96-12374-1
; Sequence 1, Application PC/TUS9612374
; GENERAL INFORMATION:
; APPLICANT: Northwestern University
; TITLE OF INVENTION: Herpes Virus Entry Mediator
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Dressler, Goldsmith, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12374
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Northrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: NOR3446P020PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5400
; TELEFAX: (312) 616-5460
; TELEX: --
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 294..1145
; NAME/KEY: mat_peptide
; LOCATION: 294..1142
; PCT-US96-12374-1
; Query Match 99.1%; Score 87.3; DB 5; Length 1724;
; Best Local Similarity 99.4%; Pred. No. 3.2e-228;
```

Matches 876; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 cctgagacatgagacccctctgagagactgagagcctctccctctgagatcacccccagaa 60
   |||
Db 286 CCGAGGACATGAGACCTCTGAGAGACTGGGGGCTCTCTCTGAGATCCACCCCGAGAA 345
   |||

QY 61 ccgagctcttgagagctgltgltatctacactctcctgagagccccctgtaagccccag 120
   |||
Db 346 CCGAGCTCTGAGAGCTGCTGCTGATCTCACTCTCTGGAGGCCCTGCTAGGCCCCAG 405
   |||

QY 121 ctctgcccctctcgaagagagagagagagagagagagagagagagagagagagagag 180
   |||
Db 406 CTCTGCGCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
   |||

QY 181 gtcacaggtatctgtgaagagagagagagagagagagagagagagagagagagagag 240
   |||
Db 466 GTCCAGGTTATCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
   |||

QY 241 gccctccagagacactatctgacacactcaatgagcctaagagagagagagagagagag 300
   |||
Db 526 GCCCTCCAGAGACCTACATGATGCTCCACCTCAATGAGCCTAAGCAAGTGTCTGAGCCAA 585
   |||

QY 301 tctgtgagacacagagagagagagagagagagagagagagagagagagagagagagag 360
   |||
Db 586 TGTGTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
   |||

QY 361 tctgtgtgagacacagagagagagagagagagagagagagagagagagagagagagag 420
   |||
Db 646 TGTGTGTGCTGACACCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
   |||

QY 421 gccgcgttaccgacacactcagagagagagagagagagagagagagagagagagagagag 480
   |||
Db 706 GCCGCGCTTACGCGACACTCCAGCCCGGGCCAGAGGGGTGAGAGAGAGAGAGAGAGAGAG 765
   |||

QY 481 aggaacacccctgtctgagaactgcccccgagagagagagagagagagagagagagagag 540
   |||
Db 766 AGGACACCTGTGTGAGAACTGCCCCCGGGGAGACTTCTCTCCAAAGAGAGAGAGAGAG 825
   |||

QY 541 aatgtacagacacagacacagagagagagagagagagagagagagagagagagagagag 600
   |||
Db 826 AATGTACAGACACAGACCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
   |||

QY 601 gctccacagtgatgtgtgttctctcagagagagagagagagagagagagagagagagag 660
   |||
Db 886 GCTCCACAGTGTGATGTGTGTCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 945
   |||

QY 661 caattgtgactaatcatatgtgtgaagagagagagagagagagagagagagagagagag 720
   |||
Db 946 CAGTTGTGCTTAAATCATATGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
   |||

QY 721 tctgtccctcagagagagagagagagagagagagagagagagagagagagagagagagag 780
   |||
Db 1006 TCTGTCTCCGCTCCAGCGGAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065
   |||

QY 781 tgaagagccccctcagagagagagagagagagagagagagagagagagagagagagagag 840
   |||
Db 1066 TGAAGAGCCCCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125
   |||

QY 841 gtagagagagagagagagagagagagagagagagagagagagagagagagagagagag 881
   |||
Db 1126 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1166
   |||

```

RESULT: 2

```

US-08-266-080B-12
; Sequence 12, Application US/08266080B
; Patent No. 5606031
; GENERAL INFORMATION:
; APPLICANT: Jack Lile
; APPLICANT: Tadahiko Kohno
; APPLICANT: Duane Bonam
; APPLICANT: Mary S. Rosendahl
; TITLE OF INVENTION: Production of Biologically Active

```

```

; TITLE OF INVENTION: Recombinant Neurotrophic Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266, 080B
; FILING DATE: 27-JUNE-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,122
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/087,912
; FILING DATE: 06-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/680,681
; FILING DATE: 04-APRIL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/594,126
; FILING DATE: 09-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/547,750
; FILING DATE: 02-JULY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/505,441
; FILING DATE: 06-APRIL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: SYNE200C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; US-08-266-080B-12

```

Query Match 6.8%; Score 59.6; DB 1; Length 691;
Best Local Similarity 49.7%; Pred. No. 2.4e-07;
Matches 180; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

```

QY 164 gtagtcccccaatgtagtccagagagagagagagagagagagagagagagagagagagag 223
   |||
Db 228 GTGCTTCAGACCAAGTCTCGCCCGGCGCAACATGCAAAAGTCTTGTGACCAAGAGAGAG 287
   |||

QY 224 caagagtgtgaacccctgcccctcagagagagagagagagagagagagagagagagagag 283
   |||
Db 288 CACCGTGTGAGACTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 347
   |||

QY 284 gtagtgcagtgccaatgtgtgaagagagagagagagagagagagagagagagagagagag 343
   |||
Db 348 GTGCTTGAGACTGTGG---CTCCCGCTGTAGCTGTGACCAAGTGTGAAGAGAGAGAGAGAG 404
   |||

QY 344 cagagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 403
   |||
Db 405 TCGGAGACAGAAACGATGTGACCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 464
   |||

QY 404 ggaacactgagcagcgtgagcagcttaccgacacactcagagagagagagagagagagagag 463
   |||

```


[illegible]

RESULT 3
PCT-US95-05423-12

	Query Match	6.8%;	Score 59.6;	DB 5;	Length 691;
	Best Local Similarity	49.7%;	Pred. No. 2.4e-07;		
	Matches 180;	Conservative	0;	Mismatches 179;	Indels 3; Gaps 1
OY	164 gttctgtccccaagatgcagtcacgattatcgtgtgaagaaggacctcgaggagtcaaggg	223			
Db	228 GTGCTGCAGACGAAGTCTCCCGGGCCAAATCATAAAGTTCTTGACCAGAACCCCGGA	287			
OY	224 caccatgtgtgaacctctgcccccacaagcaaccatacttgcaccactcaatgygctaagcaa	283			
Db	288 CACCGGTGTGACTCTCTGTGAAGACAAGCACATACACCAAGCTCTGGAACTGGGTTGCCAA	347			
OY	284 gtgtctgcagtgccaatltgtgtaaccaagcaatgggacctgcgacgagccygaactgtctc	343			
Db	348 GTGCTTGAGCTGTGG---CTCCCGGTGTAGTCTGTGACAGGTGAAGAATCAAGCCCTGCAC	404			
OY	344 caggacagagaagacgcgcgt	403			
Db	405 TCGGGAAACGAAGACCGCATTCCTGTGCACCTGTGCAGGGCCCGGCTGTACTGTGGCGCTTAAGCAAGA	464			
OY	404 gaaccactgcgcgcgctgtgcgcgtttagcagcacaccctccaaagccccgggacagaaggtgcagaa	463			
Db	465 GGAGGGGTGCCCGCTGTGTGGCGCCCGCTGTGGCAAGTAGTGCSCCGCGGGCTTGTGGGTGTGGCCAG	524			
OY	464 ggagaggcaaccgaagatcagggaacaccttgtttagaactgtcccccgagggaacctctctcc	523			
Db	525 ACCGAGAACTGAATCATCAGACGTGGTGTGCAAGGCCCTGTGCCCGGGGACACTTCTCCAA	584			
OY	524 ca 525				
Db	585 CA 586				

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05423
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/266,090
 FILING DATE: 27-JUNE-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/240,122
 FILING DATE: 09-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/087,912
 FILING DATE: 06-JULY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/680,681
 FILING DATE: 04-APRIL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/594,126
 FILING DATE: 09-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/547,750
 FILING DATE: 02-JULY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/505,441
 FILING DATE: 06-APRIL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: SYME200/PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 691 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US95-05423-12

RESULT 4
 US-08-385-229-3
 Sequence 3, Application US/08385229
 Patent No. 5605690
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Cindy A.
 APPLICANT: Smith, Craig A.
 TITLE OF INVENTION: Method of Treating TNF-Dependent
 TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/385,229
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/946,236
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wight, Christopher L.
 REGISTRATION NUMBER: 31,680
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 587-0606
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1557 base pairs


```

RESULT 6
US-08-650-000-1
; Sequence 1, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,000
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,453
; FILING DATE:
; APPLICATION NUMBER: US/08/038,765
; FILING DATE:
; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,635
; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Fibroblast
; CLONE: WI-26 V44
; IMMEDIATE SOURCE:
; LIBRARY: WI-26 V44
; CLONE: 1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1473
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1470
; FEATURE:

```

```

; NAME/KEY: sig_peptide
; LOCATION: 88..153
; PUBLICATION INFORMATION:
; AUTHORS: Smith, Craig A.
; AUTHORS: Davis, Terri
; AUTHORS: Anderson, Dirk
; AUTHORS: Solam, Lisabeth
; AUTHORS: Beckmann, M. P.
; AUTHORS: Jerzy, Rita
; AUTHORS: Power, Steven K.
; AUTHORS: Cosman, David
; AUTHORS: Goodwin, Raymond G.
; TITLE: A Receptor for Tumor Necrosis Factor Defines
; TITLE: an Unusual Family of Cellular and Viral Proteins
; JOURNAL: Science
; VOLUME: 248
; PAGES: 1019-1023
; DATE: 25-MAY-1990
; US-08-650-000-1

Query Match 6.6%; Score 58; DB 2; Length 1641;
Best Local Similarity 49.4%; Pred. NO. 8.8e-07;
Matches 179; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

QY 164 gtgtgtccccaagtgcagtcacagtlacgtgtgaaggagcctgcgggagctgaaggg 223
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 GTGCTGACGAAGTCTCGCGCGGCCCAACATGCAAGTCTTGTCACGAACCTCGCA 302
QY 224 cacagltgtgaacctgcctccacagaccctacattgcacacctaatgtgctaagaa 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 303 CACCGTGTGACCTCTGTGAGACACACATACCCACCTGTGAACCTGAGTCCCGA 362
QY 284 gtgtgtcagtgccaatgtgtgacccagccatggcgctgcggcgagcgaactctc 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 363 GTGCTT---GAGCTGTGCTCCCGCTTACTCTGACACAGGTGAACCTGAAGCTGCAC 419
QY 344 cagacagagacagcgcgtgtgtgtgacagccagccacattcgtacgtccagagcg 403
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 420 TCGGGAACAGAACCGCATCTGCACACTGCAGGCCGCTGTGACTGCCGCTGACGA 479
QY 404 ggaaccactgcgcgcgtgcgcgttaccgcaacctcagcccgaggcagaggtgcagaa 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 480 GGAAGGGTGCGCGCTGTGCGCGCGCTGCGCAAGTGCCTGCGCGGCTTCGCGGCGCAG 539
QY 464 gggagggacccgagagtgtagaacacccctgttcgaactgcccccgaggacctcttc 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 540 ACCAGAACTGAACATCAAGACGTGTGCAAGCCTGTGCCCCGGGAGCTTCTCAA 599
QY 524 ca 525
    ||
DB 600 CA 601

RESULT 7
5395760-1
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:1:

```



```

RESULF 11
US-08-477-733B-4
; Sequence 4, Application US/08477733B
; Patent No. 5981724
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,733B
; FILING DATE: June 07, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; IMMEDIATE SOURCE:
; CLONE: CD40 EXTRACELLULAR REGION
; US-08-477-733B-4

```

```

Matches 190:  Conservative  0:  Mismatches 192:  Indels  9:  Gaps  1:
OY  130  cctgcagaaggaggaagctaccagctggtgctccgagttgctgtgcccaagtgcagtcaggtt 189
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   16  CATGCAGAGAAATAAACAGTAAATTAACAGTCAGTGCCTTTCTTTGTGCCAGCCAGGC 75
OY  190  atcgtgtgaagaagagccttcgscgsgagcctgcagcgacagtgctgtgaacccttcctcag 249
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   76  AGAAACGGTGGTGTACTGCTACACAGAGTTCTACTGAAACGGAAAGCCCTTCTTGCGGTGANA 135
OY  250  gcacctatacttccccacctcaatgacctaaagcaagtgctcgtgagtcgccaatgtgtgacc 309
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   136  GCGAATTCCTAGTACACACTGGAAACAGAGACACACTGCCACACAGCAAAATTACTCGAAC 195
OY  310  cagccatggtgcctgcgcgcgagccggaactgtctccaagacagagaagacgcggtgtgtgtt 369
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   196  CCAACCTTAGGGGCTTGCGGCTCCAGCAGAAAGGGGCACCTCAGAAACACAGACCAATCTCACC 255
OY  370  gcagcccgagggccactctctgcatactgcaccggaagggagaccactgcgcgcggtgtgcgctt 429
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   256  GTGAAGAAAGGCGCTGGCAGCTGTACAGTGAAGGCTGTGAAGCTGTCTCTGCACCCCTAT 315
OY  430  acgcgaactccagcccgagccagaggtgcagaaaggagacagcagagtcagagacc 489
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   316  GCTC-----GCCCGGCTTTGGGGGTCAAGCAATTTGCTACAGGGGTTTGTATACCA 366
OY  490  tgtgtcagaactgcgcccccgggagacctctc 520
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   367  TCTGCGAGCCCTGCCAGTCGGCTTCTTCTC 397

RESULT 12
US-09-088-913A-4
; Sequence 4, Application US/0908913A
; Patent No. 6087329
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,913A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:

```

Query Match	6.3%	Score 55.8	DB 3	Length 519
Best Local Similarity	48.6%	Pred. No. 2.3e-06		
Matches 190; Conservative	0;	Mismatches 192;	Indels 9;	Gaps 1

RESULT 13
US-08-602-791-1
; Sequence 1, Application US/08602791
; Patent No. 6074836

APPLICANT: BORDIGNON, Claudio
APPLICANT: MAVILIO, Fulvio
TITLE OF INVENTION: METHOD OF MARKING EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKIADO, MARTELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W.,
STREET: Suite 330 - G Street Lobby
CITY: Washington
STATE: DC

[illegible]

RESULT 14
US-08-762-308-11
Sequence 11, Application US/08762308
Patent No. 5923548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
APPLICANT: Bazzoni, Piavia M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: USA
;; ZIP: 77210-4433
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/762,308
;; FILING DATE: 09-DEC-1996
;; CLASSIFICATION: 530
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/224,593
;; FILING DATE: 05-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kitchell, Barbara S.
;; REGISTRATION NUMBER: 33,928
;; REFERENCE/DOCKET NUMBER: UTSD:335--1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 418-3000
;; TELEFAX: 474-7577
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3796 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-762-308-11

Query Match 5.2%; Score 46.2; DB 2; Length 3796;
Best Local Similarity 48.1%; Pred. No. 0.0019;
Matches 194; Conservative 0; Mismatches 203; Indels 6; Gaps 2;

QY 126 ccgtccgcgaaggagagcggtaccagtggtccgagtcgcccgaagtgcaccca 165
DB 163 CAGATCTCACAGGAATATCTATGACAGGAAGGCTCAGATGCTGCTAGTCTCTCT 222
QY 186 ggtatcgtgtgaagagagcgctcgaggaagctgaaggaagtggtgaacctgcct 245
DB 223 GGGCAATATGTGAACATTTCTGCAACAACACTCGACACCGTGTGCGGACTGTGAG 262
QY 246 ccaggaacctacattgcacacctcaatgagcctaagcaagtgtctgcaagtgccaaatgt 305
DB 283 GCAAGCATGTATACCCAGGCTGTGGAACCACTTCTGTACATGTTTGAAGCTGC--AGTTCT 339
QY 306 gaccacagcatggtgctgcgcgcgagcggaactgtctccagagacagaagcgcgtgtgt 365
DB 340 TCTGTATACACTACAGGATGAGATCCGGCTGCACCTAAACAGACGAGTGTGT 399
QY 366 ggttcgagccagagcactctgcatcgtccaggaaggg--gaccactgcgcgcgtgc 422
DB 400 GCTTGGCAAGCTGGCAGTACTGCGCTTGAACCACTTCTGACACTTTCACACTGC 459
QY 423 cgcgcttaagccacactccagccgagccagagaggtgcagaagaggaagcaccgaagtcag 482
DB 460 ATGAGGCTGAGCAAGTGCGGCTCTGGCTTGGAGTGGCCAGTTCAGAGCCCAATATGA 519
QY 483 gacacacctgtgtcagaactgc 525
DB 520 AATGTGCTATGCAAGGCTGTGCTGCCAGGAGCGTCTCTGACA 562

RESULT 15
US-08-650-000-3
; Sequence 3, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:

;; APPLICANT: Smith, Craig A.
;; APPLICANT: Goodwin, Raymond G.
;; APPLICANT: Beckmann, M. Patricia
;; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: U.S.A.
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/650,000
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,453
;; FILING DATE:
;; APPLICATION NUMBER: US/08/038,765
;; FILING DATE:
;; APPLICATION NUMBER: US 403,241
;; FILING DATE: 05-SEP-1989
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 405,370
;; FILING DATE: 11-SEP-1989
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 421,417
;; FILING DATE: 13-OCT-1989
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 523,635
;; FILING DATE: 10-MAY-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wright, Christopher L.
;; REGISTRATION NUMBER: 31,680
;; REFERENCE/DOCKET NUMBER: 2501-D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 587-0430
;; TELEFAX: (206) 233-0644
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3813 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: mouse
;; STRAIN: C57BL/6
;; CELL TYPE: T-helper cell
;; CELL LINE: 7B9
;; IMMEDIATE SOURCE:
;; CLONE: 11
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 55..1479
;; FEATURE:
;; NAME/KEY: mat_peptide
;; LOCATION: 121..1476
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 55..120
;; US-08-650-000-3

Query Match 5.2%; Score 46.2; DB 2; Length 3813;

Best Local Similarity 48.1%; Pred. No. 0.0019;
Matches 194; Conservative 0; Mismatches 203; Indels 6; Gaps 2;

```
QY 126 ccgctccgcaaggaggaagataccagtggtccgagtgctgcccgaagtgcagtcoca 185
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 CAGATCTTCACAGGAAATACATAGACAGGAAGGCTCAGATGTGCTGTGCTAACTGTCTCT 234
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 ggtatcgtgtgaaggagggcctgcgggagctgacgggacagtggtgaaacctgcacct 245
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 GGCCAAATATGTGAACAATTTCTGCAACAAGACTCGGACACCGTGTGTGCGGACTGTGAG 294
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 246 ccaggcaacttaattgcccactcactcaatggtcctaaagtgctgcagtgccaaatglt 305
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 GCAAGCATGTATACCCAGAGTCTGGAACCAAGTTTGTATATGTGTGAGCTGC---AGTTCT 351
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 306 gaccagcagcatgggcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 365
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 352 TCTGTACCACTGACACAGTGGAGATCCGCGCTGCACTAAACAGACAGAACCGAGTGTGT 411
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 366 ggttgcaagccagggcaactctgcatgctccaggaagcggg---gaccactggtccgcgtgc 422
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 412 GCTTGCGAAGCTGGCAGGTACTGCGCCCTTGAAACCCATTCTGCGAGCTGTGACAGTGC 471
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 423 cgcgcttaagccaccctccagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 482
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 472 ATGAGGCTGAGCAAGTGGCGCCCTGCGCTTCGAGTGGCGAGTCAAGAGCCCCCAATGGA 531
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 483 gacacccctgtgtcgaactgccccccgggggacactctctccca 525
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 532 AATGTGCTATGCAAGGCTGTGCCCCAGGGACGTTCTGTGACA 574
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: April 24, 2001, 18:41:23
Job time: 12235 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd..

OM nucleic - nucleic search, using sw model

Run on: April 24, 2001, 17:12:21 ; Search time 1027.86 Seconds
(without alignments)
6006.262 Million cell updates/sec

Title: US-08-741-095b-25

Perfect score: 881

Sequence: 1 cctgagcagtgagcctcct.....ccacagactctgaccccca 881

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 segs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

13: gb_est13:*

14: gb_est14:*

15: gb_est15:*

16: gb_est16:*

17: gb_est17:*

18: gb_est18:*

19: gb_est19:*

20: gb_est20:*

21: gb_est21:*

22: gb_est22:*

23: gb_est23:*

24: gb_est24:*

25: gb_est25:*

26: gb_est26:*

27: gb_est27:*

28: gb_est28:*

29: gb_est29:*

30: gb_est30:*

31: gb_est31:*

32: gb_est32:*

33: gb_est33:*

34: gb_est34:*

35: gb_est35:*

36: gb_est36:*

37: gb_est37:*

38: gb_est38:*

39: gb_est39:*

40: gb_est40:*

41: em_estba:*

42: em_estfun:*

43: em_esthum1:*

44: em_esthum2:*

45: em_esthum3:*

46: em_esthum4:*

47: em_esthum5:*

48: em_esthum6:*

49: em_esthum7:*

50: em_esthum8:*

51: em_esthum9:*

52: em_esthum10:*

53: em_esthum11:*

54: em_esthum12:*

55: em_esthum13:*

56: em_esthum14:*

57: em_esthum15:*

58: em_esthum16:*

59: em_esthum17:*

60: em_esthum18:*

61: em_esthum19:*

62: em_esthum20:*

63: em_estin1:*

64: em_estin2:*

65: em_estin3:*

66: em_estin4:*

67: em_estov1:*

68: em_estov2:*

69: em_estp11:*

70: em_estp12:*

71: em_estp13:*

72: em_estp14:*

73: em_estp15:*

74: em_estro1:*

75: em_estro2:*

76: em_estro3:*

77: em_estro4:*

78: em_estro5:*

79: em_estro6:*

80: em_estro7:*

81: em_estro8:*

82: em_estro9:*

83: em_estro10:*

84: em_estro11:*

85: em_estro12:*

86: em_estro13:*

87: gb_est41:*

88: gb_est42:*

89: gb_est43:*

90: gb_est44:*

91: gb_est45:*

92: gb_est46:*

93: gb_est47:*

94: gb_est48:*

95: gb_est49:*

96: gb_est50:*

97: gb_est51:*

98: gb_est52:*

99: gb_est53:*

100: gb_est54:*

101: gb_est55:*

102: gb_est56:*

103: gb_est57:*

104: gb_est67:*

105: gb_est68:*

106: gb_est69:*

107: gb_est70:*

108: gb_est71:*

109: gb_est72:*

110: gb_est73:*

111: gb_est74:*

112: em_esthum21:*

113: em_esthum22:*

114: em_esthum23:*

115: em_estom1:*

116: em_estom2:*

117: em_estp16:*
 118: em_estp17:*
 119: em_estp18:*
 120: em_estp19:*
 121: em_estp20:*
 122: em_estp21:*
 123: em_estp22:*
 124: em_estp23:*
 125: em_estp24:*
 126: em_estp25:*
 127: em_estp26:*
 128: em_estp27:*
 129: em_estp28:*
 130: em_estp29:*
 131: em_estp30:*
 132: em_estp31:*
 133: em_estp32:*
 134: em_estp33:*
 135: em_estp34:*
 136: em_estp35:*
 137: em_estp36:*
 138: em_estp37:*
 139: em_estp38:*
 140: em_estp39:*
 141: em_estp40:*
 142: em_estp41:*
 143: em_estp42:*
 144: em_estp43:*
 145: em_estp44:*
 146: em_estp45:*
 147: em_estp46:*
 148: em_estp47:*
 149: em_estp48:*
 150: em_estp49:*
 151: em_estp50:*
 152: em_estp51:*
 153: em_estp52:*
 154: em_estp53:*
 155: em_estp54:*
 156: em_estp55:*
 157: em_estp56:*
 158: em_estp57:*
 159: em_estp58:*
 160: em_estp59:*
 161: em_estp60:*
 162: em_estp61:*
 163: em_estp62:*
 164: em_estp63:*
 165: em_estp64:*
 166: em_estp65:*
 167: em_estp66:*
 168: em_estp67:*
 169: em_estp68:*
 170: em_estp69:*
 171: em_estp70:*
 172: em_estp71:*
 173: em_estp72:*
 174: em_estp73:*
 175: em_estp74:*
 176: em_estp75:*
 177: em_estp76:*
 178: em_estp77:*
 179: em_estp78:*
 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	453	51.4	493	93	AM630737
2	400.2	45.4	796	135	BE728963
3	376.8	42.8	523	137	BE891768
4	348.6	39.6	589	1	AA020847
5	311.4	35.3	532	89	AM72968
6	281.2	31.9	428	4	AA262421
7	271	30.8	457	1	AA021617
8	267	30.3	823	19	AI356409
9	244	27.7	482	107	BE386504
10	240	27.2	556	8	AA481843
11	228.8	26.0	251	7	AA426526
12	218.6	24.8	719	21	AI479005
13	213.6	24.2	426	2	AA088363
14	211.4	24.0	237	111	BE699740
15	203.2	23.1	682	97	AM78536
16	203.2	22.0	304	4	AA293583
17	194.2	22.0	262	135	BE770179
18	187	21.2	274	147	AA2185
19	178.8	20.3	672	111	BE676441
20	176	20.0	627	108	BE465035
21	153	17.4	892	13	AA890591
22	151	17.1	565	24	AI765809
23	148	16.8	606	92	AM590114
24	146.4	16.6	506	1	AA018179
25	139.4	15.8	641	13	AA934011
26	127.8	14.5	597	92	AM590183
27	124.4	14.1	597	105	BE221308
28	119.8	13.6	510	11	AA722732
29	76.4	8.5	560	105	BE234440
30	75.2	8.5	449	14	AA987435
31	71.8	8.1	191	1	AA015831
32	70	7.9	520	27	AI989788
33	69.6	7.9	581	25	AI794181
34	60.2	6.8	375	133	BE014983
35	57	6.5	595	137	BE908916
36	55.8	6.3	484	142	N25156
37	55.4	6.3	576	93	AM657964
38	55.4	6.3	871	3	AA203290
39	53.8	6.1	576	106	BE285979
40	53.8	6.1	639	107	BE375846
41	53.8	6.1	679	3	AA207651
42	52.4	5.9	821	16	AI119599
43	52.2	5.9	500	38	AM012145
44	52.2	5.9	732	87	AM211419
45	51.6	5.9	393	97	AM934924

ALIGNMENTS

RESULT 1
 AM630737
 LOCUS
 DEFINITION
 AM630737 493 bp mRNA
 hb86h04.y1 NCI-CGAP CUI Homo sapiens cDNA clone IMAGE:2969719 5'
 similar to TR:Q92956 Q92956 HERPESVIRUS ENTRY MEDIATOR. ;, mRNA
 sequence.
 AM630737
 VERSION
 AM630737.1 GI:7377527
 EST
 AM630737
 EST
 AM630737.1 GI:7377527

Source	Organism	Human
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 493)	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Chris Mokaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: image.llnl.gov/image/html/iresources.shtml Seq primer: -40RP from Glbco High quality sequence stop: 400. Location/Qualifiers 1..493 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2969719" /clone_id="NCI_CGAP_G01" /tissue_type="2: pooled high-grade transitional cell tumors" /lab_host="DH10B" /note="Organ: genitourinary tract; Vector: pCMW-SPORT; Site_1: Salt; Site_2: Nci; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies.." BASE COUNT 112 a 144 c 156 g 81 t ORIGIN	
Query Match	51.4%; Score 453; DB 93; Length 493;	
Best Local Similarity	94.9%; Pred. No. 8.6e-104;	
Matches 468; Conservative	0; Mismatches 25; Indels 0; Gaps 0;	
Db 1	GTGTGGTGTGACGCCAGCCACTTCTGTGATGTGCAGACAGGGGACCTCTCGCGCGCTG	
422	ccggagcttagccacacccctccagcccgggcacaaggtgtaagaaggagacacagagatca	
61	CCGGGCTTACCCCACTCCACCCCGGGCCAAAGGGTGCAGAAGGAGGACCGACGAGATCA	
482	ggacacctgtgtcagaactgcccccggggagacctctctccaaatggagacctgtgagga	
121	GGACACCCTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGAAGA	
542	atgtcagcaccagaccaaagtgcagctgtgtgtgtaagaaagccggagcttggagccagag	
181	ATGTACAGCACCAGCAAAAGTGCACCTGCTGTGACGAAAGCCGGAGCTGGGACACAG	
602	ctccacactgggtatgtgtgttctctcaaggagaccttgatctgtcatgttcttcac	
241	CTCCACACTGGGTATGTGTGTCTCTCTCAGGAGCCTCTCATTCGTCATTTGTTGCTCAC	
662	agttggacctaatcatatgtgtgaaagaagaagccaagggtgtgtgtacgaagttgat	
301	AGTTGGCCTATTCATATGTGTGCAAAAAGCAAAAGCCAAAGGGGTGATGTAGTCAAGTAT	
722	cgctccgttcacagcgaaagacagagagcgaaagtgtgaagccacacgaftcatltgagccct	
361	CGTCTCCGCCGACGAGAAAGACAGAGAGGTGAGAGCCACACGATTTGAGAGGCC	
782	gcagagcccttcggaagctcaccacggtgtggtccgtgtgaggaagaataacctcatcaagg	

Db	421	TGCACCCCTCCCGACGTACACCGAGGAGGAGCATGAGACATATACGTTATTCACGGG	480
Qy	842	gaggagcccaaac	854
Db	481	GAGAACCGCAAC	493
RESULT	2		
LOCUS	BE728963	796 bp	EST
DEFINITION	601562209p1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831818 5',		15-SEP-2000
ACCESSION	BE728963		
VERSION	BE728963.1	GI:10142955	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 796)		
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC/DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: L10CM508 row: a column: 03 High quality sequence start: 10 High quality sequence stop: 681. Location/Qualifiers		
FEATURES			
source	1..796		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3831818"		
	/clone_11b="NIH.MGC.20"		
	/tissue_type="melanotic melanoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	135 a	267 c	234 g
ORIGIN	160 t		
Query Match	45.4%;	Score 400.2;	DB 135; Length 796;
Best Local Similarity	91.9%;	Pred. No. 1.8e-90;	
Matches 501; Conservative	0;	Mismatches 33;	Indels 11; Gaps 7;
Qy	1	cctgaggaatgagactctctgagagcttgggggcttccctcgagagatccaccaga	60
Db	237	CCTGAGGATGAGAGCTCTCGAGAGCTGGGGGCTCTCTCCGAGATCCACCCAGAA	296
Qy	61	ccgaagctttagagctgtgtctgtatctcaacttctgagagcccccctagccccc	120
Db	297	CCGAGCTTTGAGCTGGTGGCTGTATCTACCTCTCTGGAGACCCCTCTAGCCCCG	356
Qy	121	ctctgcgctctctgcaagagagagtaaccacagtgagcttcgagtgctgccccaa	180
Db	357	CTCTGCGCTCTCTGCAAGAGAGGACGAGTACCCAGTGGCTCCGAGTGTCTCCCA	416
Qy	181	gtccaagttatctgtgtgaagagagccctcggggagagctgaagggacacagtgt	240

Db 417 GTCCAGTTATCGTGAAGAGAGCGCTGCGGGAGCTGACGGGACACAGTGTGTAACCT 476

QY 241 gccctcagagacctaacttgcccaaccatgacctaagaagtgtctgaagtgccaa 300
 |||||
 Db 477 GCCCTCCAGGGA-CTACATGCCCCAC--TCATAGGCTAGAGAGTGTGCAAGTCCAAA 533
 |||||

QY 301 tctgtgaccagcagatgagctgcgcgcag--ccgaactctccagagcagaagacc 359
 |||||
 Db 534 TGTGTAGACCCAGGACATGGGCGCGGAGACCGGAGACTCTCCAGGACAGAGACGCC 593
 |||||

QY 360 gtgtg-tgtgtcagccagagccactctgcatcgtccagagcaggagaccatgcgcgc 418
 |||||
 Db 594 GTGTGTGGCTGACAGCCGAGGACACTTCTGATGCTCAGAGACGGGACCACTGCGCGG 653
 |||||

QY 419 gtgcgcagcttaacccacccctcagcccgagaggtgcaagaggagaccagag 478
 |||||
 Db 654 GTGCCGGCTTACGCCAC--TCCAGCCGGGCGGAGAGGTCGACAGC--AGGACCGAGAG 709
 |||||

QY 479 tcagagacacccctgtcgaactgcccccgaggacctctctcccaatggagacctgga 538
 |||||
 Db 710 TCAGGACACCTGTTTGAAGATGGCCCC--GGGACCTTTTCCCATGGGACCTGAG 767
 |||||

QY 539 ggaat 543
 |||

Db 768 GAATT 772

RESULT 3
 BE891768 523 bp mRNA EST 29-SEP-2000
 LOCUS BE891768 601434494F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919655 5',
 DEFINITION mRNA sequence.
 ACCESSION BE891768
 VERSION BE891768.1 GI:10351422
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: ATCC/DCMP/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1CM736 row: 1 column: 24
 High quality sequence stop: 522.
 Location/Qualifiers
 1..523
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="3919655"
 /clone_lib="NIH_MGC_72"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."
 BASE COUNT 88 a 169 c 167 g 95 t 4 others
 ORIGIN

Query Match 42.88; Score 376.8; DB 137; Length 523;
 Best local similarity 98.14; Pred. No. 1.3e-84;

Matches 413; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

QY 1 cctgagcatggaacccctcctggagacgagggcctctccttgagatccaccocagaa 60
 |||||
 Db 103 CTTAGGACATGACCTCTCGAGAGCTGGGGGCTCTCTCCCTGAGATCCACCCAGAA 162
 |||||

QY 61 ccgacgctcttgagctgtgtctatctcaactctcctggagagccctctgtaagccag 120
 |||||
 Db 163 CCGAGCTCTTGAAGCTGTGTGTATCTCACTTCTGGGAGGCCCTGCTACGCCAG 222
 |||||

QY 121 ctctgcgtctctgaagaggaagtaaccagtgaggctccagatgtctgcccaatgca 180
 |||||
 Db 223 CTCTGCGCTCTCTGCAAGAGAGGAGTACAGTACAGTGGGCTCCGATGCTGCCCAAGTGA 282
 |||||

QY 181 gtccaggttctgtgtgaagagagcctgcggagagcgtgaagagcagtggtgaacct 240
 |||||
 Db 283 GTCCAGGTTATCGTGAAGAGAGGCTGCGGGAGCTGACGGGACAGTGTGAACCT 342
 |||||

QY 241 gccctcagagacctaacttgcccaactcaatggccttaagcaagtgc--tgcaatgcca 298
 |||||
 Db 343 GCCCTCAGGACCTACATTTGCCACCTCAATGGCCTAAGCAAGTGTGAGTCCCA 402
 |||||

QY 299 aa--tgtgtgacccagcatg--ggctgcgcgcagagccggaactgtctcagagagaa 335
 |||||

Db 403 NAATGTTGTGACCCAGCCAGCTGCGCGGAGCCGAGCCGGAAGCTGCCAGAGAGAA 462
 |||||

QY 356 gcgcgtgtgtgtgagagccagagccactctgcatcgtccagagagagacactgcgc 415
 |||||

Db 463 CGCGGTGTGTGCTGCAAGCCAGGCGCACTTCTGATGCTCCAGGACGGGACCACTGCGC 522
 |||||

QY 416 c 416
 |

Db 523 c 523

RESULT 4
 AA020847 589 bp mRNA EST 30-JAN-1997
 LOCUS AA020847 266401.r1 Soares retina N2b4HR Homo sapiens cDNA clone
 DEFINITION IMAGE:363721 5', mRNA sequence.
 ACCESSION AA020847
 VERSION AA020847.1 GI:1484618
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapelli, B.,
 Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, M., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
 Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Warr, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1574 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 462.
 Location/Qualifiers
 1..589
 /organism="Homo sapiens"
 /db_xref="GDB:1280424"
 /db_xref="taxon:9606"

```

/clone="IMAGE:363721"
/clone_id="Soares retina N2B4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: eye; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTACCAATCTGAGTGGAGCGCGCGCGGTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M. Fatima Bernaldo."

```

```

BASE COUNT      117 a      182 c      183 g      104 t      3 others
ORIGIN
Query Match      39.6%; Score 348.6; DB 1; Length 589;
Best Local Similarity 94.1%; Pred. No. 1.7e-77;
Matches 449; Conservative 0; Mismatches 19; Indels 9; Gaps 8;

```

```

Oy 7 gcatgagacccctgagagactgggggctctccctgtagatcaaccccgagacg 66
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 GGATGGACCCCTGGAAGACTGGGGGCTCTCCCTGGAGATCAACCCCAAAACCGACG 166

Oy 67 tcttgaagctgctgctgctatctcaactctcctggagagccctctgtaagcccaagctg 126
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 TCTTGAGGCTGCTGTGTATCTCACTCTCTGGAGAGCCCTGCTAGGCCCCAGCTCTGC 226

Oy 127 cgtctgcaagagagagagatcaccagtggtgctcagagtgctgcccgaagtga- 185
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 CGTCTGCAAGAGAGACAGTACCCAGTGGGCTCCGAGTCTGCCCAAGTGCANGTCCA 286

Oy 186 ggttatcgtgtggaagagagctctgaggga--gctgaagcgagacagtgtgttaaccc 243
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 GGTATCTGTGGAAGAGAGCTGCGGGAGACTGACCGGACAGTGTGTAACCCCTGCC 346

Oy 244 ctcc-aggaccatcatgcccacactcaatgagcctaagcagtgctcagtgccaatg 302
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 CTCGAAGCCTACTTACATTTGCCACCTCAATGAGCTTAAGCAAGTGTCTCAATGCA 406

Oy 303 tgtgacccagcagctggtgctgctgagcgagacactgctcagagacagagacgctg 362
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 407 TGTGACCCAGCATTTGGGCTGCGGCGGAG--CGGAAGTCTCTCAGAGACAGAACGCCGTG 465

Oy 363 tgtgtgtgagacccagcagcactctgcatgctcagagagcgagacactgcccgtg 422
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 466 TGTGCTGTGCAAC--CGAGGCACTTCTGTGATCTGT--CAAGAAAGGGGAAACATGCGCGCGTGC 523

Oy 423 cgcctttagcaccctcagcgcgagcgaggtgtagaagagagagagacagagagt 479
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 524 CG-GCTTAAGCAACTTCAAGCCCGGG--CAAAAGTGTGCAAGAGGAGAGACAGAGAGT 578

```

```

RESULT 5
LOCUS AM372968 532 bp mRNA EST 04-FEB-2000
DEFINITION QV3-PT0382-171299-043-g07 BT0382 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM372968
VERSION AM372968.1 GI:6877622
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS HGCP http://www.ludwig.org.br/ORESTES.

```

```

TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV3&t2=QV3-BT0382-
171299-043-g07&t3=1999-12-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 532.
Location/Qualifiers
1. 532
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="BT0382"
/dev_stage="Adult"
/notes="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

```

```

BASE COUNT      108 a      155 c      182 g      87 t
ORIGIN

```

```

Query Match      35.3%; Score 311.4; DB 89; Length 532;
Best Local Similarity 98.1%; Pred. No. 3.8e-68;
Matches 315; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Oy 1 cctgaagcatagagacccctcctgagagagcctcctccctgtagatcaaccccgag 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 402 CCTGAGCATAGAGACCTCTGGAAGCTGGGGCTCTCACTGAGATCAACCCCGAGAA 343

Oy 61 ccgacgtctgagagctgctgctgctatctcaactctcctgtagagccctctgtaagcc 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 342 CCGAGCTTTGAGGCTGCTGTATCTCACTCTCTGGAGAGCCCTGCTAGGCCCCAG 283

Oy 121 cctgcccctcgaagagagagatcaccagtggtgctcagagtgctgcccgaagtga 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 282 CTCTGCCGTCTGCAAGAGAGAGACAGTACCCAGTGGGCTCCGAGTCTGCCCAAGTGA 223

Oy 181 gtccaggtatcgtgtgaagagagcctgctgagagcctgagagcgagcagtgtagaac 240
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 222 GTCCAGGTTATCTGTGAGAGAGGCTGCGGGAGCTGTGAGCGGACAGTGTGAACCT 163

Oy 241 gccctcagagacactatctgcccacactcaatgagcctcaagcagtgctcagtgccaa 300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 GCCCTCAGGACCTTAATTTGCCACCTCAATGSCCTTAAGCAAGTGTCTGAGTGCATA 103

Oy 301 tgtgtgacccagccatgagcc 321
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 102 TGTGTGACCCAGTTAAGAGGC 82

```

```

RESULT 6
LOCUS AA262421 428 bp mRNA EST 13-AUG-1997
DEFINITION z517604.r1 NCI-GCB1 Homo sapiens cDNA clone IMAGE:685470 5'
similar to TR:G1167929 G1167929 ORF U144.1; mRNA sequence.
ACCESSION AA262421
VERSION AA262421.1 GI:1897917
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

REFERENCE 1 (bases 1 to 428)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 COMMENT Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1528 Std Error: 0.00
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 405.

FEATURES
 Source

1. 428
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:685470"
 /clone_1lb="NCI CGAP GCBI"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20⁺, 19D⁺),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CEBR). cDNA synthesis was
 primed with a Not I - oligo(dt) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCTTCAATTTTTTTTTTTT-3',
 1. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 78 a 141 c 128 g 81 t

Query Match 31.9%; Score 281.2; DB 4; Length 428;
 Best Local Similarity 97.4%; Pred. No. 1.5e-60;
 Matches 339; Conservative 0; Mismatches 3; Indels 6; Gaps 5;

Db 7 gcatggagccctcgtgagactgggggctcctcccttgagatccacccagagacgagc 66
 |||||||
 Db 87 GCATGGAGCCCTCTGGAGACTGGGGGCTCTCTCTGAGATCCACCCCAAGACCGACG 146
 |||||||
 QY 67 tcttgagagctgtgtctatctacacctctgtagagccctgctacgcccagctctgc 126
 |||||||
 Db 147 TCTTGAGAGCTGTGCTGTATCTACCTTCCTGGAGGCCCTGCTACGCCCTCCTGCG 206
 |||||||
 QY 127 cgtctcgaaggaagagagatccagctggctcgcagctgctgcccagaatgacgtcag 186
 |||||||
 Db 207 CGTCTCTCCAA-CAGGAGAGATACC--AGTGGCTCCGAGTGGTCCCAAGTCAAGTCAG 263
 |||||||
 QY 187 gttatcgttgaagaagagagcctcgtgagagctgaagggcacaagtgttgaacccgcctc 246
 |||||||
 Db 264 GTTATCTGTGAAGAGAGCCCTGGCGGAGCTGAGCGGACACAGTGTGAACCTGCGCTC 323
 |||||||
 QY 247 caggcacctacatgtccacacctcaatgacctaaagaagtgtctcagtgccaagtgtg 306
 |||||||
 Db 324 CA-GCAGCTACATGTGCCACCTCAATGGCTTAAGCAAGTGTCTCATGTCCCAATGTGTG 382
 |||||||
 QY 307 accagcactggagctgcgcgcgagcccggaactgtctccagagacagaga 354
 |||||||
 Db 383 ACCGAGCAT-GGCTCTGGCGGCA-CGGAACCTGCTCCAGAGACAGAGA 428

RESULT 7
 AA021617 457 bp mRNA EST 30-JAN-1997
 LOCUS
 DEFINITION z669d02.r1 Soares retina N2b4HR Homo sapiens cDNA clone

IMAGE:364227 5', mRNA sequence.
 AA021617 GI:1485315
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 457)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, M., Harkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Martis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Riklin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevas, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Merritt, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

JOURNAL MEDLINE

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1546 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 364.

FEATURES

Source

1. 457
 /organism="Homo sapiens"
 /db_xref="GDB:1280930"
 /db_xref="taxon:9606"
 /clone="IMAGE:364227"
 /clone_1lb="Soares retina N2b4HR"
 /sex="male"
 /tissue_type="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pRT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dt) primer [5'
 TGTTCACCAATCTGAAGTGGAGCGCGCTTCAATTTTTTTTTT 3'],
 TGTTCACCAATCTGAAGTGGAGCGCGCTTCAATTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRT73 vector
 (Pharmacia). The retinas were obtained from a 55 year old
 Caucasian and total cellular poly(A)⁺ RNA was extracted 6
 hrs after their removal. The retina RNA was kindly
 provided by Roderick R. McInnes M.D. Ph.D. from the
 University of Toronto. Library constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 83 a 145 c 135 g 86 t 8 others

Query Match 30.8%; Score 271; DB 1; Length 457;
 Best Local Similarity 94.8%; Pred. No. 5.5e-58;
 Matches 330; Conservative 0; Mismatches 12; Indels 6; Gaps 5;

QY 7 gcatggagccctcgtgagactgggggctcctcccttgagatccacccagagacgagc 66
 |||||||
 Db 107 GATGGAGCCCTCTTGAGAGCTGGGGGCTCTCTCTGAGATCCACCCCAAGACGAGC 166
 |||||||
 QY 67 tcttgagagctgtgtctatctacacctctgtagagccctgctacgcccagctctgc 126
 |||||||
 Db 167 TCTTGAGAGCTGTGCTGTATCTACCTTCCTGGAGGCCCTGCTACGCCCTCCTGCG 226
 |||||||
 QY 127 c-gtctcgaaggaagagagatccagctggctcgcagctgctgcccagaatgacgtcag--tc 183
 |||||||
 Db 227 CAGTCTGCAAGGAGGAGGAGTACCCAGTGGCTCCGAGTGTGCCCCCAAGTCAAGTCC 286

QY 184 caggtatcatcgtgtaag-aggcctcgcggagcctgacggacagctgtgtgaacctg 242
 |||||
 Db 287 AAGGTTATCGTGTGAAGAAAGCTGCGGGAGCTGACGGGACAGTGTGTGACCCCTGC 346
 |||||
 QY 243 cctccaggaacctacattgcccacctcaatgagcgaagtgtctgagtgccaatg 302
 |||||
 Db 347 CCTCAGGACCTACATGTCCTCCACCTCAATGAGCTTACAGTGTGTGTGAGCCCAATG 406
 |||||
 QY 303 -tgtagccagcagctgctgcgc-gcgagcggagactgtcccaaga 348
 |||||
 Db 407 TTGTACCCAGCATGGCTGCGGCGACCGGAGACTGCTCCAGGA 454
 |||||
 RESULT 8
 LOCUS A1356409 823 bp mRNA EST 16-FEB-1999
 DEFINITION qz26g11.x1 NCI-CGAP.CLI1 Homo sapiens cDNA clone IMAGE:2028068 3' similar to TR:Q92956 Q92956 HERPESVIRUS ENTRY MEDIATOR. ; mRNA sequence.
 ACCESSION A1356409
 VERSION A1356409
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 823)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnlnl.gov/dbp/image/image.html
 Insert Length: 1470 Std Error: 0.00
 Seq primer: -40UP from Gidco
 High quality sequence stop: 454.
 FEATURES
 source
 Location/Qualifiers
 1..823
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2028068"
 /clone_id="NCI-CGAP.CLI1"
 /tissue_type="B-cell, chronic lymphocytic leukemia"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pec (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGGAGGAGCGCGCATGCTGTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73D vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 150 a 257 c 245 g 168 t 3 others
 ORIGIN
 Query Match 30.3%; Score 267; DB 19; Length 823;
 Best Local Similarity 86.8%; Pred. No. 6.1e-57;
 Matches 328; Conservative 0; Mismatches 46; Indels 4; Gaps 3;
 QY 504 ccccgaggacctctcccaatgagacctgaggaatctgacacacacgaatgac 563
 |||||
 Db 821 cccccccggcgtttttcccaatgagacctgaaagagtcagaccgacccagctgac 762

QY 564 agctgctgtgtgacgaagcccgagcctgagccacgaactccacatgggtatgtgtt 623
 |||||
 Db 761 AGCCTGCTGTGTACAGAGGCGCCAGACTGG--ACAGCACTTNCATGGTATGGTGT 704
 |||||
 QY 624 ctctcaggaagcctcgtcatcgtcattgttgtctccacagttgacctaatatgtgtg 683
 |||||
 Db 703 CTTCAAGGAGAGCTGTCAATGCTCATGTGCTCCACAGTGGGCTAATATATGTGTG 644
 |||||
 QY 684 aaaaagaagaagccaaaggggtgtagtgaagtgtatcgtctccgtccagcggaaga 743
 |||||
 Db 643 AAAAGAAAGAAAGCCAAAGGGGTGATGTACTCAAGGTGAT-GTCTCATCCACCGAAAGA 585
 |||||
 QY 744 cagagagcagaaggtgagggccacagctttagagccctcgagccctcgagctacc 803
 |||||
 Db 584 CAGGAGGCAAGAGGTGAGGCGCCACAGTGTAGGCGCTGCAAGCCCTCCGAGCT -ACC 526
 |||||
 QY 804 acggtgacctgagagagacaataaccctcattcaacggagagagcccaaacactgacc 863
 |||||
 Db 525 ACGGTGCGCGTGGAGAGACATATACCTCATTCACGGGAGAGAGCCCAACCACTGACCC 466
 |||||
 QY 864 acagactctgaccccgga 881
 |||||
 Db 465 ACAGACTCTGCACCCCGA 448
 |||||
 RESULT 9
 LOCUS BE386504 482 bp mRNA EST 21-JUL-2000
 DEFINITION 601273744.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614650 5', mRNA sequence.
 ACCESSION BE386504
 VERSION BE386504
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 482)
 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: ATCC/DCTP/DRP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnlnl.gov/plate.LCM277 row: h column: 11
 High quality sequence start: 7
 High quality sequence stop: 480.
 FEATURES
 source
 Location/Qualifiers
 1..482
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3614650"
 /clone_id="NIH_MGC_20"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: Vector; POTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 69 a 173 c 137 g 103 t
 ORIGIN

were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 53 a 84 c 36 t

Query Match 26.0%; Score 228.8; DB 7; Length 251;
Best Local Similarity 96.8%; Pred. No. 2.1e-47;
Matches 244; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 256 acattgccaccatcattgagcctgaagcagtcctcagtcgcaatgtgtgaccagcca 315
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 ACATTGACACCTCTAATGGCTTAAGCAAGTCTCTGCACTGCCAATGTGTACCCAGCCA 60
OY 316 tgggcttcgagcagcagcagcagcagtcctcagagagagaaagccgltgtgttcagcc 375
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 TGGGCTGCGGCGAGCGGAGAACTGCTCCAGACAGAGAAAGCCGCTGTGTGTGAG-C 119
OY 376 cagcaccatttcgctcagtcagagagagagcagcagtcgctgctgcagcagcca 435
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 120 CAGGCACTTCTGTCATGCTCAGAGAGCGGAGCACTGCGCGCGCGCATACGCCA 179
OY 436 cctcagcccgagcagagagtgacagagagagcagcagagtcagagaccctgtgtc 495
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 180 CCTCAGCGCCGCGGCGAGAGGTCGAGAGAGGAGGACCGAGAGTCAAGACCTGTGTCT 239
OY 496 agaactgcccc 507
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 240 AGAAGTGGCCCC 251

RESULT 12
A1479005/c 719 bp mRNA EST 14-APR-1999
LOCUS tm29f10.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2158027 3'
DEFINITION similar to TR:Q92956 Q92956 HERPESVIRUS ENTRY MEDIATOR.;; mRNA
sequence.

ACCESSION A1479005 GI:4372173
VERSION A1479005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Insert Length: 1356 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 455.

FEATURES

1. 719
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2158027"
/clone_lib="NCI_CGAP_CLL1"

BASE COUNT 138 a 228 c 211 g 141 t 1 others

Query Match 24.8%; Score 218.6; DB 21; Length 719;
Best Local Similarity 95.2%; Pred. No. 9e-45;
Matches 257; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

OY 612 gatagtgtgttcctcagagagcctcgtcagtcagtcattgttgcctcagagtgcccta 671
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 719 GTATGGGTGTTTCTCTAGGAAAGCTGTCTCATCTATTGTTTGTCTCCAGTTGGCCCTA 660
OY 672 atcatatgttgaaagaaagaaagcagagagtgatgtatgtatgtatgtatgtatgtatgt 731
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 659 ATCATATGTGTG-AAAGAAAGAAAGCCAAAGGGTGATGTAGTCAAGGTGATC-TCTCCGTC 602
OY 732 cagcagaaag 791
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 601 CAGCGG-AAAG 543
OY 792 ccgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 851
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 542 CCGGAGCTCACACAGGTGGCGCGTGAGAGACATATACCTCATTCAGCGGAGAGAGCCCA 483
OY 852 aaccactgacccaagacactctgaccccca 881
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 482 AACCACTGACCCACAGACTCTGCACCCCGA 453

RESULT 13
AA088363 426 bp mRNA EST 24-OCT-1996
LOCUS 2182C02.r1 StrataGene colon (#937204) Homo sapiens cDNA clone
DEFINITION IMAGE:511106 5', mRNA sequence.
ACCESSION AA088363 GI:1633875
VERSION AA088363
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 426)
JOURNAL Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
MEDLINE Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
GENE M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Morris, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

CONTACT: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28W13 rev2 from Amersham
High quality sequence stop: 269.

FEATURES

Location/Qualifiers

Plate: 394
Seq primer: Forward.

FEATURES
Location/Qualifiers
source 1. .682

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE ressequences, MAGP"
/note="Vector: pBluescriptskm"

BASE COUNT 123 a 219 c 205 g 135 t
ORIGIN

Query Match 24.0%; Score 211; DB 97; Length 682;

Best Local Similarity 95.6%; Pred. No. 7.3e-43;

Matches 217; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
OY 655 gctcacagcttggcctaatactatgtgtgaaagaagccaagggtgtagtca 714
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 682 GCTCCAGTTCGGCTTAATCATATGTGTGANAAGATAGCCAAGGGGTGATGATCA 623

OY 715 agtgcacgtctccgtccagcgcgaagaacagagagcagaagtcgagccacagtcattg 774
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 622 AGGTGATGTCTCTCCGTCCAGCGGAAGACAGAGGCGAAGGTGAGGCCACAGTCATTG 563

OY 775 aggcacctgcagggccctccgcgaacgtcacacgctgcgcgtgagagagaacaatacctcat 834
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 562 AGGCCTGTGCAGGCCCTCCGAACGTCAACCGCGTGTGAGAGAGACAATACCTCAT 503

OY 835 tcacggggagagagcccaaacactgcagcccaagactctgcaccccgga 881
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 502 TCACGGGGAGAGCCCAAACCACTGACCCACAGACTTTGCACCCCGA 456
```

Search completed: April 24, 2001, 19:23:30
Job time: 7869 sec

THIS PAGE IS BLANK (RECEIVED)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 17:31:39 ; Search time 17.99 Seconds

(without alignments)
899.233 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 1578
Sequence: 1 MEPPGDMPPMRSTPRIDV.....VTVAVETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_0401.*
2: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
18: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
23: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1578	100.0	283	17 W05809	Human tumour necro
2	1578	100.0	283	19 W69238	Herpesvirus entry
3	1578	100.0	283	20 Y06488	Human tumour-asso
4	1578	100.0	283	21 Y94721	Human TR2-receptor
5	1578	100.0	283	21 Y93695	Amino acid sequenc
6	1578	100.0	283	21 Y95348	Human PRO509 anti
7	1575	99.8	283	19 W67045	Human TNF receptor
8	1575	99.8	283	20 W87591	Human tumour necro
9	1575	99.8	283	21 Y94717	Human TR2-receptor
10	1572	99.6	283	20 W95031	Tumour necrosis fa
11	1570	99.5	283	18 W12659	Human herpes simpl

12	1570	99.5	283	20 Y05797	Herpes virus entry
13	1373.5	87.0	277	21 Y79207	Membrane-bound her
14	1068	67.7	193	21 Y79204	Soluble herpesvitu
15	1060	67.2	197	21 Y79205	Soluble herpesvitu
16	1058	67.0	186	21 Y79206	Soluble herpesvitu
17	604.5	38.3	185	19 W60046	Human TNF receptor
18	604.5	38.3	185	21 Y94716	Human TR2-receptor
19	604.5	38.3	240	17 W05810	Human TNF receptor
20	393	24.9	166	19 W60047	Human TNF receptor
21	393	24.9	166	21 Y94719	Human TR2-receptor
22	377.5	23.9	134	17 W05811	Human tumour necro
23	332	21.0	278	21 Y95322	Pig costimulatory
24	276.5	17.5	281	21 Y94715	Murine CD40 protei
25	268.5	17.0	277	20 Y32191	CD40 protein. Uni
26	267.5	17.0	276	20 Y33499	Human CD40 protein
27	267.5	17.0	277	14 R38859	CD40 protein. Hom
28	267.5	17.0	277	20 Y52701	Human CD40 protein
29	267.5	17.0	277	22 B50520	Human tumour necro
30	267.5	17.0	277	22 B37807	Human CD40. Homo
31	260	16.5	325	13 R27865	Rabbit fibroma vir
32	260	16.5	325	16 R85071	Shope fibroma viru
33	260	16.5	461	16 R72504	p75 Tumour Necrosi
34	259	16.4	183	16 R77421	BamP delta53 nerv
35	259	16.4	225	21 Y77463	Primate protein se
36	259	16.4	235	19 W59665	Human soluble tumo
37	259	16.4	235	19 W52270	Tumour necrosis fa
38	259	16.4	235	20 W89234	Tumour necrosis in
39	259	16.4	235	21 Y54441	Amino acid sequenc
40	259	16.4	235	21 Y54443	Wild type N-termin
41	259	16.4	235	22 B37685	Human 40 KDa TNF I
42	259	16.4	248	21 Y94718	Human type 2 tumou
43	259	16.4	461	12 R11001	40KD TNF inhibitor
44	259	16.4	461	12 R11141	Human TNF-R deduce
45	259	16.4	461	14 R42058	Fibroblast derived

ALIGNMENTS

RESULT	1
ID	W05809
W05809	standard; Protein; 283 AA.
AC	W05809;
XX	
DT	30-JUN-1997 (first entry)
XX	
DE	Human tumour necrosis factor receptor.
XX	
KW	Human; tumour necrosis factor; TNF; receptor; treatment;
KW	activation; inhibition; identification; agonist; antagonist;
KW	stimulation; T cell; differentiation; mediation; immune;
KW	antiviral; response; regulation; growth; protection; HIV;
KW	radiation; Chlamydia; infection; immunodeficiency; virus;
KW	autoimmune disease; inflammation; septic shock; cerebral;
KW	cachexia; B cell; cancer; graft; host; reaction; rejection;
KW	prevention; apoptosis; cytotoxicity; hybridisation probe;
KW	detection; antibody; reagent.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Peptide 1..38
FT	/label= sig_peptide
FT	Peptide 39..283
FT	/label= mat_peptide
XX	
PN	W09634095-A1.
XX	
PD	31-OCT-1996.
XX	
PE	27-APR-1995; 95MO-US05058.
XX	

PR 27-APR-1995; 95MO-US05058.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz R, NI J, Rosen CA;
 XX
 DR WPI: 1996-497627/49.
 DR N-PSDB; T40048.
 XX
 PT New nucleic acid encoding a human tumour necrosis factor receptor -
 PT useful for treatment of auto-immune diseases etc., in diagnosis and
 PT for drug screening
 XX
 PS Claim 1; Pages 47-48; 73pp; English.
 XX
 CC The present sequence is the human tumour necrosis factor (TNF)
 CC receptor, which may be used for the identification of TNF receptor
 CC agonists or antagonists. TNF receptor agonists inhibit tumour
 CC growth, stimulate cell (e.g. T cell) differentiation, mediate the
 CC immune and antiviral responses, regulate growth, protect against
 CC radiation and Chlamydia infection, and can be used to treat
 CC immunodeficiencies, e.g. human immunodeficiency virus. Antagonists
 CC can be used to treat T cell mediated autoimmune disease.
 CC Inflammation, septic shock, cerebral malaria, cachexia or B cell
 CC cancers, to inhibit graft-host reactions and to prevent apoptosis
 CC or cytotoxicity. Fragments of the TNF receptor encoding DNA can be
 CC used as hybridisation probes for detecting related genes.
 CC Antibodies against the protein can be used as reagents for
 CC detecting/measuring soluble forms of protein in the circulation.
 XX
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 17; Length 283;
 Best Local Similarity 100.0%; Pred. No. 3.4e-121;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPPGDMGPPMRSTPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVSECCPKCSPG 60
 DB 1 meppgdmgppmrstprtldvlrlvlylflgapyapalpsckedeypvseccpkcspg 60
 QY 61 YRVKACGELGTIVCEPCPPGTITIAHLNGLSKLQCCOMCDPAMGLASRNCSTENAVCG 120
 DB 61 yrvkaacgeltgtivcepcppgtityahlnnglskclqccomcdpamglasrncstenaavcg 120
 QY 121 CSPGHFCTIVODGDHCAACRAVATSSPGQRVQKGTESQDTLQONCPRTGSPNGLTEECQ 180
 DB 121 cspghfctivodgdhcaacrayatsspgqrvqkgtesqdtlqoncpptglsngtleecq 180
 QY 181 HQTKCSWLTKAGAGTSSSHMMWMLFSGSLVIYVCTVGLITICVRRKPRGDPVAVIYS 240
 DB 181 hqtkswlvtkagagtssshmmwmlfsgslviyvcstvglltcvrrkprgdvavkiys 240
 QY 241 VQKRGAEAGEATVIALQAPPDVTVAVEETIPSTGRSPNH 283
 DB 241 vqkrgaeageatvialqapdpvtvaveetipstgrspnh 283
 RESULT 2
 ID W69238 standard; Protein; 283 AA.
 XX
 AC W69238;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Herpesvirus entry mediator protein.
 KW Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
 KW gene expression regulator; cellular stress; inflammatory response;
 KW lymphocyte activity regulator; autoimmune response.
 XX
 OS Homo sapiens.

XX
 PN W09825967-A1.
 XX
 PD 18-JUN-1998.
 XX
 PF 05-DEC-1997; 97MO-US22278.
 XX
 PR 12-DEC-1996; 96US-0032705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Marsters SA;
 XX
 DR WPI: 1998-348457/30.
 DR N-PSDB; V44852.
 XX
 PT Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in
 PT assays for HVEM and to produce antibodies and transgenic animals,
 PT e.g. for drug screening
 XX
 PS Claim 1; Fig 1; 46pp; English.
 XX
 CC This sequence is the herpesvirus entry mediator (HVEM) protein of
 CC the invention. The protein is useful in quantitative diagnostic assays
 CC for HVEM, in affinity purification of HVEM from recombinant cells/natural
 CC sources and in competitive-type receptor binding assays. It can also be
 CC used to generate antibodies, also useful in diagnostic assays for HVEM
 CC and affinity purification of HVEM. HVEM is believed to be a member of the
 CC tumour necrosis factor receptor (TNFR) family, and transient transfection
 CC of HVEM into human 293 cells caused marked activation of certain
 CC transcription factors, e.g. AP-1, suggesting that HVEM is involved in
 CC regulating gene expression in response to infectious stimuli and cellular
 CC stress. The predominant expression of HVEM mRNA in lymphocyte-rich
 CC tissues (e.g. spleen and peripheral blood) also suggested it may be a
 CC receptor in regulating lymphocyte activity. Antibodies produced may be
 CC therefore be useful therapeutically, e.g. antagonistic antibodies may be
 CC e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM
 CC regulation of such induction. The DNA may be used diagnostically, e.g.
 CC to determine if DNA and/or RNA encoding HVEM is present in cells, and to
 CC prepare HVEM polypeptide recombinantly. It is also useful to produce
 CC non-human transgenic animals (e.g. mice or rats), especially knockout
 CC animals containing cells with an altered gene encoding HVEM polypeptide.
 CC Such animals are useful in the development and screening of
 CC therapeutically useful reagents.
 XX
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 19; Length 283;
 Best Local Similarity 100.0%; Pred. No. 3.4e-121;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPPGDMGPPMRSTPRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVSECCPKCSPG 60
 DB 1 meppgdmgppmrstprtldvlrlvlylflgapyapalpsckedeypvseccpkcspg 60
 QY 61 YRVKACGELGTIVCEPCPPGTITIAHLNGLSKLQCCOMCDPAMGLASRNCSTENAVCG 120
 DB 61 yrvkaacgeltgtivcepcppgtityahlnnglskclqccomcdpamglasrncstenaavcg 120
 QY 121 CSPGHFCTIVODGDHCAACRAVATSSPGQRVQKGTESQDTLQONCPRTGSPNGLTEECQ 180
 DB 121 cspghfctivodgdhcaacrayatsspgqrvqkgtesqdtlqoncpptglsngtleecq 180
 QY 181 HQTKCSWLTKAGAGTSSSHMMWMLFSGSLVIYVCTVGLITICVRRKPRGDPVAVIYS 240
 DB 181 hqtkswlvtkagagtssshmmwmlfsgslviyvcstvglltcvrrkprgdvavkiys 240
 QY 241 VQKRGAEAGEATVIALQAPPDVTVAVEETIPSTGRSPNH 283
 DB 241 vqkrgaeageatvialqapdpvtvaveetipstgrspnh 283


```

RESULT 3
ID Y06488 standard; Protein; 283 AA.
XX Y06488:
AC 27-SEP-1999 (first entry)
XX
XX Human tumour-associated protein PRO509.
DE
XX PRO1112; UNQ555; cancer; tumour necrosis factor receptor;
XX diagnosis; therapy; human.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 201..225
XX /note= "transmembrane domain"
XX Domain 226..283
XX /note= "cytoplasmic domain"
XX
XX W09935170-A2.
XX
XX 15-JUL-1999.
XX
XX 05-JAN-1999; 99W0-US00106.
XX
XX 20-NOV-1998; 98US-0109304.
XX 05-JAN-1998; 98US-0070440.
XX 29-APR-1998; 98US-0083500.
XX 22-MAY-1998; 98US-0086414.
XX 10-JUN-1998; 98US-0088742.
XX 10-NOV-1998; 98US-0107783.
XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
XX Roy MA, Wood WI;
XX WPI: 1999-430385/36.
XX N-PSDB: X87265.
XX
XX Antibody against proteins expressed in neoplastic cells, useful for
XX tumor diagnosis and treatment
XX
XX Example 1; Fig 24; 162pp; English.
XX
XX This sequence represents human PRO509 (UNQ329), a protein encoded
XX by the novel cDNA clone DNA50148 (see X87264), and a member of the
XX tumour necrosis factor receptor family. Amplification of DNA50148
XX was observed in various tumour tissues, suggesting a role in tumour
XX formation or growth. Antagonists (e.g. antibodies) directed to
XX PRO509 may have use in cancer therapy. The invention identifies
XX 14 genes (see X87254-67) that are amplified in the genome of tumour
XX cells. Such amplification is expected to be associated with
XX overexpression of the gene product and to contribute to tumorigenesis.
XX The encoded proteins (see Y06477-90) may be useful targets for the
XX diagnosis and/or treatment (including prevention) of certain cancers,
XX and may act as predictors of the prognosis of tumour treatment.
XX Antibodies that bind the proteins are claimed and used in claimed
XX cancer diagnostic kits.
XX
XX Sequence 283 AA;

```

Query Match 100.0%; Score 1578; DB 20; Length 283;
 Best Local Similarity 100.0%; Pred. No. 3.4e-121;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPPGDMPGPPMRSPRDLVRLVLTFLGAPCYAPALPSCSKDEVPVSGCCPKKSPG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MPPGDWPPPPWSTPDLVRLVLTFLGAPCYAPALPSCSKDEVPVSGCCPKKSPG 60

```

OY 61 YRVKACGELTGTVCPCPPGTIAHLNGLSKCLQCGWCDPAMGLRARNCSRTENAVCG 120
|||
DB 61 YRVKACGELTGTVCPCPPGTIAHLNGLSKCLQCGWCDPAMGLRARNCSRTENAVCG 120
OY 121 CSPGHFCTIVQDGDHCAACRAVATSSPGORVOKGGETESODTLQCNCPETGSPNLTLECCQ 180
|||
DB 121 CSPGHFCTIVQDGDHCAACRAVATSSPGORVOKGGETESODTLQCNCPETGSPNLTLECCQ 180
OY 181 HQTGCSMLVTKAGAGTSSSHVWMMFLSGSLVTVVCSVGLITCVKRRKPRGDVVKVYVS 240
|||
DB 181 HQTGCSMLVTKAGAGTSSSHVWMMFLSGSLVTVVCSVGLITCVKRRKPRGDVVKVYVS 240
OY 241 VQRKROEAEGEATVIEALQAPPDVTVAVERTPSPFTGRSPNH 283
|||
DB 241 VQRKROEAEGEATVIEALQAPPDVTVAVERTPSPFTGRSPNH 283

RESULT 4
ID Y94721 standard; Protein; 283 AA.
XX Y94721:
XX Y94721:
XX
XX 29-JAN-2001 (first entry)
XX
XX Human TR2-receptor protein sequence.
XX
XX Tumour necrosis factor-receptor related protein; TR2; human; cancer;
XX chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
XX immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
XX severely combined immunodeficiency; apoptosis inhibition;
XX Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..38
XX /note= "Signal peptide"
XX Protein 39..283
XX /label= "TR2 receptor"
XX
XX W0200056405-A2.
XX
XX 28-SEP-2000.
XX
XX 22-MAR-2000; 2000W0-US07521.
XX
XX 22-MAR-1999; 99US-0125683.
XX 26-MAR-1999; 99US-0126522.
XX 20-MAY-1999; 99US-0135169.
XX 06-AUG-1999; 99US-0147383.
XX
XX (NIJ/) NI J.
XX (ROSE/) ROSEN C A.
XX (GENTZ/) GENTZ R L.
XX
XX NI J, Rosen CA, Gentz RL;
XX WPI: 2000-594519/56.
XX N-PSDB: A28149.
XX
XX Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
XX and its two splice variants, useful for treating arthritis or
XX inflammation, cancer (such as follicular lymphomas) and
XX immunodeficiency disorders -
XX
XX Disclosure; Page 370; 373pp; English.
XX
XX This invention relates to an isolated nucleic acid molecule encoding a
XX human tumour necrosis factor(TNF)-receptor related protein TR2. Included
XX in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
XX The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a

```

CC member of the TNFR superfamily. The invention includes a method for the
 CC treatment of arthritis or inflammation using an antibody directed against
 CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
 CC antibodies exhibit cytostatic, dermatological, antiasthmatic,
 CC immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
 CC antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
 CC cerebroprotective activity. The methods are useful for treating arthritis
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 CC preventing autoimmune diseases (such as autoimmune hemolytic anaemia,
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 CC antagonists are useful for treating or preventing autoimmune diseases and
 CC inhibit the growth, progression and/or metastasis of cancers. They are
 CC also used to activate, differentiate or proliferate cancerous cells or
 CC tissues, and can be used to treat diseases associated with increased cell
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 CC as sources for generating antibodies, as molecular weight markers.
 CC This sequence represents the TR2 receptor protein of the invention.
 XX
 SO Sequence 283 AA:

Query Match 100.0%; Score 1578; DB 21; Length 283;
 Best Local Similarity 100.0%; Pred. No. 3.4e-121;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPTDVLRLVLYLFLGAPCYAPALPSCKDEYVSGCCPKCSPG 60
 Db 1 meppgdwppwrstptdvlrlvlylflgapcyapalpsckdeyvsgccpkcspg 60
 QY 61 YRVKACGELGTGTCPCPPGTATLNLGLSKLQCCQCMCDPAMGLASRNCSTENAVCG 120
 Db 61 yrvkaacgelgtgtcpcppgtatlnlglsklqccqcmcdpamglasrncstrenavcg 120
 QY 121 CSPGHFCTIVODGDHCACRAVATSSPGRVGKGSTESDITLQNCPPGTFSPNCTLEBCQ 180
 Db 121 cspghfctivodgdhcaacravatsspgrvkgstesditlqncppgtfsgpnctleecq 180
 QY 181 HOTGCSMTYTKAGAGTSSHHWMMFLSGSLIVIVCSVGLICVKKRKPQGVKVIYS 240
 Db 181 hotgcsmtvtkagagtsshhwmmflsgslivivcsvgllcvcrrkprgdvkvivs 240
 QY 241 VQRKQAEAGATVLEALQAPPDVTVAEETIRSFTRGRSPNH 283
 Db 241 vqrkqaeagatvlealqappdvtvaveetirsftrgrspnh 283

RESULT 5
 Y93695 ID Y93695 standard; Protein; 283 AA.
 XX
 AC Y93695;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of novel polypeptide PRO509.
 XX
 KW PRO201; PRO292; PRO327; PRO1265; PRO344; PRO347; PRO357;
 KW PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 KW tumourigenesis; cancer; neoplastic cell growth; cell proliferation.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT 1..36
 FT Peptide /note="signal sequence"

FT Modified-site 81..87
 FT /note="N-myristoylation site"
 FT Modified-site 89..95
 FT /note="N-myristoylation site"
 FT Modified-site 104..110
 FT /note="N-myristoylation site"
 FT Modified-site 110..114
 FT /note="N-glycosylation site"
 FT Modified-site 120..126
 FT /note="N-myristoylation site"
 FT Modified-site 153..159
 FT /note="N-myristoylation site"
 FT Modified-site 173..177
 FT /note="N-myristoylation site"
 FT Modified-site 193..199
 FT /note="N-glycosylation site"
 FT Modified-site 195..201
 FT /note="N-myristoylation site"
 FT Domain 203..222
 FT /note="transmembrane domain"
 FT Modified-site 220..226
 FT /note="N-myristoylation site"
 FT Region 231..234
 FT /note="cell attachment sequence"

MO200037640-A2.

XX 29-JUN-2000.

PF 16-DEC-1999; 99WO-US30095.

PR 22-DEC-1998; 98US-0113296.

PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28565.

PA (GETH) GENENTECH INC.

PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;

PI Wood WI;

XX WPI; 2000-452188/39.

DR N-PSDB; A46931.

XX

PT New anti-polypeptide antibody useful in the treatment and diagnosis of

PT neoplastic cell growth and proliferation -

XX Claim 61; Fig 24; 220pp; English.

PS

XX The present sequence represents a novel human polypeptide. The

CC specification describes novel polypeptides designated PRO201, PRO292,

CC PRO327, PRO1265, PRO343, PRO347, PRO357, PRO715, PRO1017,

CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in

CC the genome of tumour cells. The polypeptides are believed to contribute

CC to tumourigenesis. The polypeptides are useful target for the

CC identification of certain cancers, and may act as predictors of the

CC prognosis of tumour treatment. Antibodies against these polypeptides

CC are useful in the treatment and diagnosis of neoplastic cell growth

CC and proliferation in mammals.

XX Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 21; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.4e-121;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPTDVLRLVLYLFLGAPCYAPALPSCKDEYVSGCCPKCSPG 60

```

Db      1 meppgdwppwrstprtdivrlvlyltflgapcyapalpsckedeypvgsccpkcspg 60
OY      1 YRVKACGELGTGVCPCPGTYIAHNLGSKLCLOCCOMCDPAMGLRASRNCSTRTENAVCG 120
Db      61 yrvkeacgelgtgvcpcpgptyiahnlglskclqcmcdpamglrasncstrenavcg 120
OY      121 CSPGHFCIVDGDHCAACRAVATSSPGQVOKGTESDTLCONCPGTSPNGTLEECQ 180
Db      121 csphfcivdgddhcaacraayatspgqvkgtesqdtlcqncppgtfsgnltleecq 180
OY      181 HOTKCSMLVTRKAGAGTSSSHWVWFLSGSLYIVVCTVGLITCYKRRKRGDVKVIVS 240
Db      181 htkcsvltvkagagtssshwwvflsgslviviavcstvglllcvkrrkprgdvkvivs 240
OY      241 VQRKQAEAGATVTEALQAPPDVTVAVEETIPSTFGSRPNH 283
Db      241 vqkrqaeagatvtealqapppdvtvaaveetlpsfgrspnh 283

RESULT 6
Y95348
ID      Y95348 standard; Protein; 283 AA.
XX
AC      Y95348;
XX
DT      25-SEP-2000 (first entry)
XX
DE      Human PRO509 antitumour protein.
XX
KW      PRO509; human; antitumour; tumour; therapy; cytostatic;
KW      breast cancer; ovarian cancer; renal cancer; colorectal cancer;
KW      uterine cancer; prostate cancer; lung cancer; bladder cancer;
KW      central nervous system cancer; melanoma; leukaemia; neoplasm.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Peptide
FT      1..36
FT      /label= signal_peptide
FT      37..283
FT      /label= PRO509
FT      Domain
FT      205..221
FT      /note= "transmembrane domain"
FT      Modified-site
FT      81..87
FT      /note= "N-myristoylation"
FT      Modified-site
FT      89..95
FT      /note= "N-myristoylation"
FT      Modified-site
FT      104..110
FT      /note= "N-myristoylation"
FT      Modified-site
FT      120..126
FT      /note= "N-myristoylation"
FT      Modified-site
FT      153..159
FT      /note= "N-myristoylation"
FT      Modified-site
FT      193..199
FT      /note= "N-myristoylation"
FT      Modified-site
FT      192..201
FT      /note= "N-myristoylation"
FT      Modified-site
FT      220..226
FT      /note= "N-myristoylation"
FT      Modified-site
FT      110..114
FT      /note= "N-myristoylation"
FT      Modified-site
FT      173..177
FT      /note= "Asn is N-glycosylated"
FT      Modified-site
FT      231..234
FT      /note= "Asn is N-glycosylated"
FT      Region
FT      /note= "cell attachment sequence"
XX
XX      WO200037638-A2.
XX
XX      29-JUN-2000.
XX
XX      02-DEC-1999; 99WO-US28565.

```

```

PR      22-DEC-1998; 98US-0113296.
PR      08-MAR-1999; 99WO-US05028.
PR      21-APR-1999; 99US-0130232.
PR      28-APR-1999; 99US-0131445.
PR      14-MAY-1999; 99US-0134287.
PR      20-JUL-1999; 99US-0144758.
PR      26-JUL-1999; 99US-0145698.
PR      15-SEP-1999; 99WO-US21090.
PR      15-SEP-1999; 99WO-US21547.
XX
PA      (GETH ) GENENTECH INC.
XX
XX      Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
PI      Napier MA, Pitti RM, Wood WI;
XX
DR      WPI: 2000-442668/38.
DR      N-PSDB; A49727.
XX
XX      Novel composition to inhibit neoplastic cell growth or for treating
PT      tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,
PT      PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or
PT      PRO866
XX
PS      Claim 19; Fig 24; 172pp; English.
XX
CC      The present sequence is that of human antitumour protein PRO509,
CC      as deduced from a retinal cDNA clone (see A49727). PRO509 shows
CC      homology to members of the human tumour necrosis factor receptor
CC      family such as the lymphotoxin-beta receptor (11 identities) and
CC      CD40 (12 identities). A claimed method for inhibiting the growth
CC      of a tumour cell comprises exposing the tumor cell to PRO179,
CC      PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526,
CC      PRO362, PRO356, PRO509 or PRO866 (see Y95337-49), their agonists or
CC      chimeric polypeptides incorporating them. The tumour is especially
CC      a cancer selected from breast, ovarian, renal, colorectal, uterine,
CC      prostate, lung, bladder and central nervous system cancer, melanoma
CC      and leukaemia. Methods for the recombinant expression of the
CC      antitumour proteins are also provided.
XX
SQ      Sequence 283 AA:

Query Match      100.0%; Score 1578; DB 21; Length 283;
Best Local Similarity 100.0%; Pred. No. 3,4e-121;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MEPPGDMGPPPMRSTPRTDVLRLVLYLTFLGAPCYAALPSCKEDYVGSSECCPKRSPG 60
Db      1 meppgdwppwrstprtdivrlvlyltflgapcyapalpsckedeypvgsccpkcspg 60
OY      61 YRVKACGELGTGVCPCPGTYIAHNLGSKLCLOCCOMCDPAMGLRASRNCSTRTENAVCG 120
Db      61 yrvkeacgelgtgvcpcpgptyiahnlglskclqcmcdpamglrasncstrenavcg 120
OY      121 CSPGHFCIVDGDHCAACRAVATSSPGQVOKGTESDTLCONCPGTSPNGTLEECQ 180
Db      121 csphfcivdgddhcaacraayatspgqvkgtesqdtlcqncppgtfsgnltleecq 180
OY      181 HOTKCSMLVTRKAGAGTSSSHWVWFLSGSLYIVVCTVGLITCYKRRKRGDVKVIVS 240
Db      181 htkcsvltvkagagtssshwwvflsgslviviavcstvglllcvkrrkprgdvkvivs 240
OY      241 VQRKQAEAGATVTEALQAPPDVTVAVEETIPSTFGSRPNH 283
Db      241 vqkrqaeagatvtealqapppdvtvaaveetlpsfgrspnh 283

RESULT 7
M60045
ID      M60045 standard; Protein; 283 AA.
XX
XX      M60045;
XX

```

DT	25-SEP-1998	(first entry)
XX		
DE	Human TNF receptor related (TR2) protein.	
KW	Human; tumour necrosis factor; TNF; herpes simplex virus;	
KW	aberrant cell survival; radiation therapy; lymphocyte proliferation;	
KW	immune deficiency syndrome.	
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FH	Peptide	1..36
FT		/note= "Signal peptide"
FT	Peptide	37..283
FT		/note= "Mature peptide"
FT	Domain	37..200
FT		/note= "Extracellular domain"
FT	Modified-site	110
FT		/note= "Asparagine-linked glycosylation site"
FT	Modified-site	173
FT		/note= "Asparagine-linked glycosylation site"
FT	Domain	201..225
FT		/note= "Transmembrane domain"
FT	Domain	226..283
FT		/note= "Intracellular domain"
XX		
PN	W09818824-A1.	
XX		
PD	07-MAY-1998.	
XX		
XX	30-OCT-1996;	96WO-US18540.
XX		
PR	30-OCT-1996;	96WO-US18540.
XX		
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	(SMIK-) SMITHKLINE BEECHAM CORP.	
XX		
PI	Genitz RL, Hurle MR, Lyn SDP, N1 J, Rosen CA;	
DR	WPI: 1998-272139/24.	
XX	N-PSDB: V34509.	
XX		
PT	Nucleic acid encoding TR2 tumour necrosis factor family receptor -	
PT	and its splice variants; useful for diagnosis and treatment of	
PT	diseases involving abnormal cell survival or death, e.g. herpes	
PT	simplex infection	
XX		
PS	Claim 1; Fig 1; 151pp; English.	
XX		
CC	The human tumour necrosis factor (TNF) receptor related protein (TR2) is	
CC	a member of the TNF family and displays considerable homology to murine	
CC	CD40. It can be used in soluble forms to treat herpes simplex virus	
CC	infection and TR2 proteins (or their agonists or antagonists) are used to	
CC	treat disease associated with aberrant cell survival. Agonists may also	
CC	be used to protect against the effects of radiation therapy and to	
CC	stimulate lymphocyte proliferation and differentiation in patients	
CC	infected by human immune deficiency syndrome.	
XX		
XX	Sequence	283 AA:
SO		
Query Match	99.8%; Score 1575; DB 19; Length 283;	
Best Local Similarity	99.6%; Pred. No. 5.9e-121;	
Matches	282; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
OY	1 MEPPDWMGPPWRSPPTDVLRLVLYLFLGAPCYAPALPSCKEDEVPGSECCPCSPG 60	
DB	1 MEGPDWPPPPRSTPKTCTVTLVLYLTLFGAPCYAPALPSCKEDEVPGSECCPCSPG 60	
OY	61 YRVKACGELTTCVCEPCPGCTGYIAHLNLSKLCQCMQCDPMGLRASNCRSTENAVCG 120	
DB	61 YRVKACGELTTCVCEPCPGCTGYIAHLNLSKLCQCMQCDPMGLRASNCRSTENAVCG 120	

Qy	121	CSBPGHCIVQDDDHCAACAVATSSSGAVKQCGTSOPLCONCPGFSSPGTLEEQ	180
Db	121	csbpghcivqdddhcaacavatsssgavkqcgtsqdlcnqcpptfsspgtleeq	180
Qy	181	HOTKCSMLTKKAGACRSSSHMMWFSLGSLVIVYICSTVGLLICVRRKPRGDVAVIYS	240
Db	181	hqtksmltkkagacrssshmmwflsgslviviycstvglllcvarrrprgdvavviys	240
Qy	241	VORKROAEGEATVIEALQAPPDVTVVAEETIPSTGSPNH	283
Db	241	vgrkrqaegeatviealqapdpvtvvaeeitpstrgsph	283
RESULT	8		
ID	W87591	W87591 standard; Protein; 283 AA.	
XX	AC		
XX	W87591;		
XX	DT	17-MAR-1999 (first entry)	
DE		Human tumour necrosis factor receptor-like 2 protein.	
XX			
KM		Tumour necrosis factor receptor-like 2; TR2. TNF; human; psoriasis;	
KM		systemic lupus erythematosus; idiopathic thrombocytopenic purpura;	
KM		rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;	
KM		insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;	
KM		atherosclerosis; viral infection.	
XX			
OS		Homo sapiens.	
XX			
PN		W09851346-A1.	
XX			
PD		19-NOV-1998.	
XX			
PE		12-MAY-1998; 98WO-US09744.	
XX			
PR		12-MAY-1997; 97US-0046249.	
XX			
PA		(SMIK) SMITHKLINE BEECHAM CORP.	
PA		(SMIK) SMITHKLINE BEECHAM PLC.	
XX			
PI		Harrop JA, Holmes SD, Reddy MP, Truneh A;	
DR	WPI; 1999-059689/05.		
DR	N-PSDB; V83763.		
PT		Method of treating pathological condition - comprises administering	
PT		tumour necrosis factor-2 antibody to patient	
XX			
PS		Disclosure; Page 27-28; 35pp; English.	
XX			
CC		This sequence represents the human tumour necrosis factor (TNF)	
CC		receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can	
CC		be used in the method of the invention to treat pathological conditions.	
CC		The method is used to treat systemic lupus erythematosus, idiopathic	
CC		thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,	
CC		psoriasis, inflammatory bowel disease, insulin-dependent diabetes	
CC		mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic	
CC		dermatitis, cancer, e.g. lymphomas and leukemias, atherosclerosis and	
CC		viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody	
CC		is also used to monitor and diagnose abnormalities in TR-2 function,	
XX		production or metabolism.	
XX			
SO	Sequence	283 AA;	
	Query Match	99.8%; Score 1575; DB 20; Length 283;	
	Best Local Similarity	99.6%; Pred. No. 5,9e-121;	
	Matches 282; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MBPDDMGCPPRKSRPRDVLRLVLYLTFLGAPCTAPALPSCKEDEYPPGSECCRCSCSG 60		

```

Db      1 meppgdwppwstlptktdvllrlvlytlflgapyapalpsckedeyvysgscpkcspg 60
Qy      61 YRVKACGELGTVCPCPGTYIAHLNGLSKLCQCCMCDPAMGLRSMRNCSTENAVCG 120
        |||
Db      61 yrvkaacgelgtvcpcpgptyiahnnglskclqccmcpamglrasncstenaavcg 120
Qy      121 CSPGHFCIVODGDHCAACRAVATSSPGQRYOKGTESDTLCONCPGTSPNGTLEECQ 180
        |||
Db      121 cspghfcivodgdhcaacrayatsspgqrvqkgtesqdtlcqncppgtfapngtleecq 180
Qy      181 HQTCSWLVTKAGAGTSSHWMMFLSGSLVIVYVCSVGLIICVKKRRKRGDVVKYIVS 240
        |||
Db      181 hqtcswlvtkagagtsesshwmmflsgslvivycstvglllcvkrrkprgdvvkylivs 240
Qy      241 VQRKROAEAGATVTEALQAPPDVTYVAEETIPSTGSRPNH 283
        |||
Db      241 vqrkrgeageatvlealqapdpvtvaaveetlpsftgspnh 283

RESULT 9
Y94717
ID      Y94717 standard; protein; 283 AA.
XX
AC      Y94717;
XX
DT      29-JAN-2001 (first entry)
XX
DE      Human TR2-receptor protein sequence.
XX
KW      Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW      Chromosome p16.2-p16.3; arthritis; inflammation; autoimmune disease;
KW      Immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
KW      severely combined immunodeficiency; apoptosis inhibition;
KW      Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Peptide
FT      1..36
FT      /note="Signal peptide"
FT      protein
FT      37..283
FT      /label="TR2 receptor"
FT      37..200
FT      /note="Extracellular domain"
FT      201..225
FT      /note="Transmembrane domain"
FT      226..283
FT      Domain
FT      /note="Intracellular domain"
XX
XX      WO200056405-A2.
XX
XX      28-SEP-2000.
XX
XX      22-MAR-2000; 2000WO-US07521.
XX
XX      22-MAR-1999; 99US-0125683.
XX      26-MAR-1999; 99US-0126522.
XX      20-MAY-1999; 99US-0135169.
XX      06-AUG-1999; 99US-0147383.
XX
XX      (NIJ/) NI J.
XX      (ROSE/) ROSEN C A.
XX      (GENT/) GENTZ R L.
XX
XX      NI J, Rosen CA, Gentz RL;
XX
XX      WPI; 2000-594519/56.
XX      N-PSDB; A28135.
XX
PT      Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT      and its two splice variants, useful for treating arthritis or
PT      inflammation, cancer (such as follicular lymphomas) and
PT      immunodeficiency disorders -

```

```

XX      Claim 1; Fig 1; 373pp; English.
PS
XX      This invention relates to an isolated nucleic acid molecule encoding a
CC      human tumour necrosis factor (TNF)-receptor related protein TR2. Included
CC      in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC      The TR2 gene is located on chromosome 1 at position p16.2-p16.3. TR2 is a
CC      member of the TNFR superfamily. The invention includes a method for the
CC      treatment of arthritis or inflammation using an antibody directed against
CC      a fragment of the TR2 protein. TR2 its agonists, antagonists and
CC      antibodies exhibit cytostatic, dermatological, antineoplastic,
CC      immunosuppressive, anti-allergic, antiarthritic, antiasthmatic,
CC      anti-inflammatory, neuroprotective, nootropic, antiparkinsonian, and
CC      cerebroprotective activity. The methods are useful for treating arthritis
CC      or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
CC      mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
CC      immunodeficiency or for enhancing an in vivo leukocyte response to an
CC      antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
CC      preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
CC      dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
CC      inflammatory myopathies) and immunodeficiency disorders (such as severely
CC      combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
CC      disorder, or Nezelof syndrome-combined immunodeficiency with Ig9). TR2,
CC      TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
CC      antagonists are useful for treating or preventing autoimmune diseases and
CC      inhibit the growth, progression and/or metastasis of cancers. They are
CC      also used to activate, differentiate or proliferate cancerous cells or
CC      tissues, and can be used to treat diseases associated with increased cell
CC      survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
CC      Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
CC      as sources for generating antibodies, as molecular weight markers.
CC      This sequence represents the TR2 receptor protein of the invention.
XX
SQ      Sequence 283 AA:

Query Match          99.8%; Score 1575; DB 21; Length 283;
Best Local Similarity 99.6%; Pred. No. 5,9e-121;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEPPGDMGPPWMSSTPRTDVLRLVLYITFLGAPCYAPALPSCKEDEVYVSSECCPKCSPG 60
        |||
Db      1 meppgdwppwstlptktdvllrlvlytlflgapyapalpsckedeyvysgscpkcspg 60
Qy      61 YRVKACGELGTVCPCPGTYIAHLNGLSKLCQCCMCDPAMGLRSMRNCSTENAVCG 120
        |||
Db      61 yrvkaacgelgtvcpcpgptyiahnnglskclqccmcpamglrasncstenaavcg 120
Qy      121 CSPGHFCIVODGDHCAACRAVATSSPGQRYOKGTESDTLCONCPGTSPNGTLEECQ 180
        |||
Db      121 cspghfcivodgdhcaacrayatsspgqrvqkgtesqdtlcqncppgtfapngtleecq 180
Qy      181 HQTCSWLVTKAGAGTSSHWMMFLSGSLVIVYVCSVGLIICVKKRRKRGDVVKYIVS 240
        |||
Db      181 hqtcswlvtkagagtsesshwmmflsgslvivycstvglllcvkrrkprgdvvkylivs 240
Qy      241 VQRKROAEAGATVTEALQAPPDVTYVAEETIPSTGSRPNH 283
        |||
Db      241 vqrkrgeageatvlealqapdpvtvaaveetlpsftgspnh 283

RESULT 10
W95031
ID      W95031 standard; protein; 283 AA.
XX
AC      W95031;
XX
DT      13-MAY-1999 (first entry)
XX
DE      Tumour necrosis factor receptor (TNF-R) related polypeptide TR2.
XX
KW      Tumour necrosis factor receptor; TNF-R; TR1; TR2; TR4; arthritis;
KW      inflammation; septicemia; autoimmune disease; transplant rejection;

```

KM graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
 KM acute respiratory disease syndrome; restenosis, bone disease; cancer;
 KM atherosclerosis; Alzheimer's disease.

OS Unidentified.

XX EP897114-A2.

XX 17-FEB-1999.

XX 04-JUN-1998; 98EP-0304424.

XX 29-AUG-1997; 97US-0057550.

XX 13-AUG-1997; 97US-0055513.

XX 26-AUG-1997; 97US-0056980.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Brigham-burke MR, Young PR;

XX WPI; 1999-134308/12.

PT Identifying agonists and antagonists to tumour necrosis factor

PT receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -

PT useful for treating stroke, Alzheimer's disease and AIDS

PS Disclosure; Page 13-14; 18pp; English.

XX The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,
 CC which cause: chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis
 CC and Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR2.

XX Sequence 283 AA;

SQ

Query Match 99.6%; Score 1572; DB 20; Length 283;

Best Local Similarity 99.6%; Pred. No. 1e-120; Mismatches 1; Indels 0; Gaps 0;

Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDYLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60

DB 1 MEPPGDMGPPWRSTPRDYLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60

QY 61 YRKVEACGELTGYCEPCPGPTTYAHLNGLSKLCQCMCPAMGLRARNCSRTENAVCG 120

DB 61 YRKVEACGELTGYCEPCPGPTTYAHLNGLSKLCQCMCPAMGLRARNCSRTENAVCG 120

QY 121 CSPGHCIVDDGDHACACRAVATSSPGORVKGSTESODPLCQCPGTSFNGTLEECQ 180

DB 121 CSPGHCIVDDGDHACACRAVATSSPGORVKGSTESODPLCQCPGTSFNGTLEECQ 180

QY 181 HQTGCSMLVTRKAGAGTSSSHMMWMLFSGSLVIVCSVGLICVKKRRKRGDVKVIVS 240

DB 181 HQTGCSMLVTRKAGAGTSSSHMMWMLFSGSLVIVCSVGLICVKKRRKRGDVKVIVS 240

QY 241 VQRKQAEAGEATVIALQAPPDVTVAVEETLPSFTGRSPNH 283

DB 241 VQRKQAEAGEATVIALQAPPDVTVAVEETLPSFTGRSPNH 283

RESULT 11

WI2659

ID WI2659 standard; Protein; 283 AA.

XX WI2659;

XX 07-MAY-1997 (first entry)

XX Human herpes simplex virus cellular mediator.

XX Herpes simplex virus cellular mediator; HHEM; receptor; HSV;

XX diagnosis; agonist; antagonist; antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..38

XX Protein 39..283

XX Region 42..75

XX Region 76..120

XX Region 121..162

XX Region 163..185

XX Region 203..225

XX Modified-site 110..112

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

XX Modified-site 173..175

Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 18; Length 283;
 Best Local Similarity 99.3%; Pred. No. 1.5e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWNRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEXPVSECCPKCSG 60
 D 1 meppgdgpppwrstprtldvrlrlvlyltflgacyapalpckedexpyvseccpkcsq 60
 QY 61 YRVEACGELTGYCEPCPGPTTYIAHLNGLSKCIQCCMCBPMGLRNRCSRTENAVCG 120
 D 61 yrvaeacgellgtvcepcpgpttyiahnglskclqccmcbpmglratncstrenavcg 120
 QY 121 CSPGHFCIVODGDHCACRAVATSSPGQRYOKGGTESODTLCONCPGTFSPNGTLEECQ 180
 D 121 csphfcivodgdhcaacrryatsspgqrvqkgtesqdlcqnccpptsngtleecq 180
 QY 181 HQTKCSWLVTKAGAGTSSHWWMFSLGSLVIVICSTVGLICVRRKRRPGDVVKYIVS 240
 D 181 hqtkcswlvtkagagtssshwwmfslgslvivicstvgllcckrrkrrpgdvvkylvs 240
 QY 241 VQKRQAEAGEATYIEALQAPPDVTVAVETIPSTFGSRPNH 283
 D 241 vqkrqaeageatylaelqapddvtlvaveetlpsftgrspnh 283

RESULT 12
 Y05797
 ID Y05797 standard; Protein; 283 AA.
 AC Y05797;
 DT 02-AUG-1999 (first entry)
 XX
 DE Herpes virus entry mediator (HVEM).
 XX
 KM Herpes virus entry mediator; HVEM; HSV receptor; infection;
 KM diagnosis; therapy; vaccine; antiviral; assay.
 XX
 OS Human herpes simplex virus.
 XX
 PN WO9920761-A2.
 XX
 PD 29-APR-1999.
 XX
 PF 22-OCT-1998; 98WO-US22342.
 XX
 PR 22-OCT-1997; 97US-0955531.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;
 XX
 DR WPI; 1999-302740/25.
 DR N-PSDB; X25512.
 XX
 FT Human herpes simplex virus receptor B5 and HVEM compositions
 PS Claim 10; Page 71-72; 89pp; English.
 XX
 CC The present sequence represents HVEM, a novel human herpes simplex
 CC virus (HSV) entry mediator that is a member of the tumour necrosis
 CC factor receptor family, and which confers on HSV the ability to
 CC infect and replicate in otherwise non-permissive cells. In the
 CC present invention, the combination of a novel porcine cell model
 CC system which is refractory to HCV entry, along with specific HSV B5
 CC (see Y05796) and/or HVEM receptor proteins enables the development
 CC of assays for screening antiviral compounds and therapeutics. The
 CC assays are useful for detecting the ability of agents to inhibit
 CC HSV entry or spread and provide for facile high-throughput
 CC screening of compounds suspected to be able to inhibit such entry,
 CC e.g. compound libraries, peptide libraries etc., to identify

CC potential drug candidates. The invention also provides a vaccine
 CC comprising the HSV receptor, an immunogenic polypeptide or
 CC fragments of the polypeptide.
 XX
 SQ Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 20; Length 283;
 Best Local Similarity 99.3%; Pred. No. 1.5e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWNRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEXPVSECCPKCSG 60
 D 1 meppgdgpppwrstprtldvrlrlvlyltflgacyapalpckedexpyvseccpkcsq 60
 QY 61 YRVEACGELTGYCEPCPGPTTYIAHLNGLSKCIQCCMCBPMGLRNRCSRTENAVCG 120
 D 61 yrvaeacgellgtvcepcpgpttyiahnglskclqccmcbpmglratncstrenavcg 120
 QY 121 CSPGHFCIVODGDHCACRAVATSSPGQRYOKGGTESODTLCONCPGTFSPNGTLEECQ 180
 D 121 csphfcivodgdhcaacrryatsspgqrvqkgtesqdlcqnccpptsngtleecq 180
 QY 181 HQTKCSWLVTKAGAGTSSHWWMFSLGSLVIVICSTVGLICVRRKRRPGDVVKYIVS 240
 D 181 hqtkcswlvtkagagtssshwwmfslgslvivicstvgllcckrrkrrpgdvvkylvs 240
 QY 241 VQKRQAEAGEATYIEALQAPPDVTVAVETIPSTFGSRPNH 283
 D 241 vqkrqaeageatylaelqapddvtlvaveetlpsftgrspnh 283

RESULT 13
 Y79207
 ID Y79207 standard; Protein; 277 AA.
 AC Y79207;
 DT 19-JUN-2000 (first entry)
 XX
 DE Membrane-bound herpesvirus entry mediator-2 (mHVEM2).
 XX
 KM mHVEM-2; membrane-bound herpesvirus entry mediator-2;
 KM TANGO-69-receptor; tumour necrosis factor receptor; human;
 KM herpes simplex virus; infection; cancer; inflammation;
 KM autoimmune disorder; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT 1..38
 FT /note="signal peptide"
 FT 39..277
 FT /note="mature protein, also separately claimed
 FT in Claim 8"
 FT 42..75
 FT /note="cysteine-rich domain"
 FT 78..119
 FT /note="cysteine-rich domain"
 FT 121..162
 FT /note="cysteine-rich domain"
 FT 165..186
 FT /note="cysteine-rich domain (partial)"
 FT 201..225
 FT /note="transmembrane domain"
 FT 110
 FT /note="N-glycosylated"
 FT 173
 FT Modified-site
 FT /note="N-glycosylated"
 PN WO200014230-A1.
 XX
 PD 16-MAR-2000.

XX 03-SEP-1999; 99WO-US20180.
 XX 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Busfield SJ;
 XX
 DR WPI: 2000-256981/22.
 DR N-PSDB; 294198.
 XX
 PT New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -
 XX
 PS Claim 8; Fig 7; 149pp; English.
 XX
 CC This polypeptide, the mature portion of which is also claimed,
 CC is human membrane-bound herpesvirus entry mediator-2 (mHVEM2); a
 CC novel form of membrane-bound herpesvirus entry mediator (mHVEM).
 CC The amino acid sequence was deduced from an isolated cDNA clone
 CC (see 294198). mHVEM2 is a TANGO-69-receptor and member of the
 CC tumour necrosis factor receptor (TNFR) superfamily. HVEM plays a
 CC role in herpes simplex virus (HSV) entry. The invention is based
 CC on the discovery of 3 cDNA molecules (see 294195-97) which encode
 CC soluble forms (see Y79204-06) of mHVEM, and the cDNA molecule
 CC encoding of mHVEM2. In addition to isolated full-length proteins
 CC and polynucleotides, and invention provides TANGO-69-receptor
 CC fusion proteins, antigenic peptides and antibodies. Also provided
 CC are recombinant expression vectors, host cells and transgenic
 CC animals in which a TANGO-69-receptor gene has been introduced or
 CC disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies
 CC can be used in screening and detection assays (e.g. chromosomal
 CC mapping, tissue typing). HVEM proteins can also be used for
 CC regulation of cell proliferation, cell differentiation, cell
 CC survival, inflammation mast cell activity, HSV infection and/or
 CC proliferation, and/or coagulation. HVEM agonists can be used to
 CC treat disorders associated with decreased HVEM activity, e.g.
 CC proliferative disorders such as carcinoma or pathogenic infection.
 CC Antagonists can be used to treat disorders associated with
 CC increased HVEM activity, e.g. autoimmune, T cell, inflammatory and
 CC allergic inflammation disorders.
 CC
 XX
 XX Sequence 277 AA:
 SQ
 Query Match 87.0%; Score 1373.5; DB 21; Length 277;
 Best Local Similarity 93.5%; Pred. No. 1.6e-104;
 Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;
 QY 1 MEPPGDMGPPMRSTPTDVLRLVLTFTGACVAPALPSCKEDEVPSSECCPKSPG 60
 DB 1 meppgdgppmrstptdvlrlvltftgacvapaalpsscckedevpssecpkspg 60
 QY 61 YRVVACGELTGTCEPCPGTYIAHNGLSKLCOCMCPAMGLRNRSCSTRENAVCG 120
 DB 61 yrvvacaageltgtcepcpgtyiahnglskclcgcmcpamglrnrscstrenavcg 120
 QY 121 CSPGHFCIVODGHCACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEECQ 180
 DB 121 cspghfcivodgdhcaacraavatsspgqvqkgtsqdtlcnpcpgtfspngtleecq 180
 QY 181 HQRKCSMLYRKAGAGTSSSHWMMFLSGSLVIVYVCTVGLIICVRRKRGDVVKYIVS 240
 DB 181 hqrcsmlyrkagagtssshwmmflsgslvivyvtvglilicvrrkrgrgdvvykivys 240
 QY 241 VQRKROEAGEATVTEALQAP 262
 DB 241 vq-----vlllplslp 253

RESULT 14
 ID Y79204
 XX Y79204 standard; Protein; 193 AA.
 XX
 AC Y79204;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Soluble herpesvirus entry mediator-1 (SHVEM1).
 XX
 KW SHVEM-1; soluble herpesvirus entry mediator-1; TANGO-69-receptor;
 KW tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..36
 FT /note= "signal peptide"
 FT Protein 37..193
 FT /note= "mature protein, also separately claimed
 FT in Claim 8"
 FT Domain 42..75
 FT /note= "cysteine-rich domain"
 FT Domain 78..119
 FT /note= "cysteine-rich domain"
 FT Domain 121..162
 FT /note= "cysteine-rich domain"
 FT Modified-site 110
 FT /note= "N-glycosylated"
 FT Modified-site 173
 FT /note= "N-glycosylated"
 FT
 XX WO200014230-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US20180.
 XX
 PR 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Busfield SJ;
 XX
 DR WPI: 2000-256981/22.
 DR N-PSDB; 294195.
 XX
 PT New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -
 XX
 PS Claim 8; Fig 1; 149pp; English.
 XX
 CC This polypeptide, the mature portion of which is also claimed,
 CC is human soluble herpesvirus entry mediator-1 (SHVEM1), a novel
 CC soluble form of membrane-bound herpesvirus entry mediator (mHVEM).
 CC The amino acid sequence was deduced from an isolated cDNA clone
 CC (see 294195). SHVEM1 is a TANGO-69-receptor and member of the
 CC tumour necrosis factor receptor (TNFR) superfamily. It is
 CC thought to play a role analogous to other soluble members of the
 CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
 CC and lymphotoxin to bind mHVEM, and to play a role in herpes simplex
 CC virus (HSV) entry. The invention is based on the discovery of 3
 CC cDNA molecules (see 294195-97) which encode soluble forms (see
 CC Y79204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd
 CC membrane-bound form (see Y79207), of mHVEM. In addition to
 CC isolated full-length proteins and polynucleotides, and invention
 CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor

CC gene has been introduced or disrupted. DNA encoding HVEM, HVEM
 CC proteins and HVEM antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVEM proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVEM
 CC agonists can be used to treat disorders associated with decreased
 CC HVEM activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVEM activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.

XX
 XX Sequence 193 AA:

Query Match 67.7%; Score 1068; DB 21; Length 193;
 Best Local Similarity 98.4%; Pred. No. 8.6e-80;
 Matches 184; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MEPPDMDGPPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
 DB 1 meppdmdgppwrstprtdvlrlvlylflgpcyapalpsckedeyvsgseccpkcspg 60
 OY 61 YRVKACGELTGTCCEPCPGTYIAHLNGLSKLCQCMCDPAMGIRASRNCSTENAVCG 120
 DB 61 yrvkacgeltgtvcepcpgtyiahlnghlskclqcmcdpamgirasncstenaavcg 120
 OY 121 CSPGHFCIVODGDHCAACRAVATSSPGRVKGGTESDITLCQNCPTSPFNGTLEECQ 180
 DB 121 cspghfcivodgdhcaacrayatsspgrvqgtesdltlcqncpptfspngtleecq 180
 OY 181 HQTCSW 187
 DB 181 hqtnraw 187

RESULT 15
 ID Y79205 standard; Protein; 197 AA.
 XX Y79205;

XX 19-JUN-2000 (first entry)
 DE Soluble herpesvirus entry mediator-2 (SHVEM2).
 XX
 KM SHVEM-2; soluble herpesvirus entry mediator-2; TANGO-69-receptor;
 KM tumour necrosis factor receptor; human; herpes simplex virus;
 KW infection; cancer; inflammation; autoimmune disorder; therapy;
 KW diagnosis.

XX Homo sapiens.

XX Location/Qualifiers
 FH Key 1..38
 FT Peptide /note= "signal peptide"
 FT Protein 39..197
 FT /note= "mature protein, also separately claimed
 FT in Claim 8"
 FT Domain 42..75
 FT /note= "cysteine-rich domain"
 FT Domain 78..119
 FT /note= "cysteine-rich domain"
 FT Domain 121..162
 FT /note= "cysteine-rich domain"
 FT Modified-site 110
 FT /note= "N-glycosylated"
 FT Modified-site 173
 FT /note= "N-glycosylated"
 XX
 XX WO200014230-A1.
 XX
 XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-US20180.
 XX 03-SEP-1998; 98US-0146950.
 PR 29-JUN-1999; 99US-0342767.
 XX
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

PI Busfield SJ;
 PT WPI: 2000-256981/22.
 DR N-PSDB: 294196.
 DR
 XX

PT New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
 PT either in the soluble or membrane bound form, is useful in screening
 PT assays and detection assays -

XX Claim 8; Fig 3; 149pp; English.

XX This polypeptide, the mature portion of which is also claimed,
 CC is human soluble herpesvirus entry mediator-2 (SHVEM2), a novel
 CC soluble form of membrane-bound herpesvirus entry mediator (mHVEM).
 CC The amino acid sequence was deduced from an isolated cDNA clone
 CC (see 294196). SHVEM2 is a TANGO-69-receptor and member of the
 CC tumour necrosis factor receptor (TNFR) superfamily. It is
 CC thought to play a role analogous to other soluble members of the
 CC TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
 CC and lymphotoxin to bind mHVEM, and to play a role in herpes simplex
 CC virus (HSV) entry. The invention is based on the discovery of 3
 CC cDNA molecules (see 294195-97) which encode soluble forms (see
 CC Y79204-06), and 1 cDNA molecule (see 294198) that encodes a 2nd
 CC membrane-bound form (see Y79207), of mHVEM. In addition to
 CC isolated full-length proteins and polynucleotides, and invention
 CC provides TANGO-69-receptor fusion proteins, antigenic peptides and
 CC antibodies. Also provided are recombinant expression vectors,
 CC host cells and transgenic animals in which a TANGO-69-receptor
 CC gene has been introduced or disrupted. DNA encoding HVEM, HVEM
 CC proteins and HVEM antibodies can be used in screening and detection
 CC assays (e.g. chromosomal mapping, tissue typing). HVEM proteins
 CC can also be used for regulation of cell proliferation, cell
 CC differentiation, cell survival, inflammation mast cell activity,
 CC HSV infection and/or proliferation, and/or coagulation. HVEM
 CC agonists can be used to treat disorders associated with decreased
 CC HVEM activity, e.g. proliferative disorders such as carcinoma or
 CC pathogenic infection. Antagonists can be used to treat disorders
 CC associated with increased HVEM activity, e.g. autoimmune, T cell,
 CC inflammatory and allergic inflammation disorders.

XX Sequence 197 AA;

Query Match 67.2%; Score 1060; DB 21; Length 197;
 Best Local Similarity 98.4%; Pred. No. 4e-79;
 Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 1 MEPPDMDGPPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
 DB 1 meppdmdgppwrstprtdvlrlvlylflgpcyapalpsckedeyvsgseccpkcspg 60
 OY 61 YRVKACGELTGTCCEPCPGTYIAHLNGLSKLCQCMCDPAMGIRASRNCSTENAVCG 120
 DB 61 yrvkacgeltgtvcepcpgtyiahlnghlskclqcmcdpamgirasncstenaavcg 120
 OY 121 CSPGHFCIVODGDHCAACRAVATSSPGRVKGGTESDITLCQNCPTSPFNGTLEECQ 180
 DB 121 cspghfcivodgdhcaacrayatsspgrvqgtesdltlcqncpptfspngtleecq 180
 OY 181 HQTCSW 187
 DB 181 hqt--nw 185

Wed Apr 25 17:48:12 2001

us-08-741-095b-26.rag

Page 12

Search completed: April 25, 2001, 17:34:32
Job time: 173 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

```
Run on:      April 25, 2001, 17:34:14 ; Search time 22.97 Seconds
              (without alignments)
              1444.050 Million cell updates/sec
```

Title:	US-08-741-095B-26
Perfect score:	1578
Sequence:	1 MPPGDWGPWPWRSTPRTDV.....VTVVAVEETIPSFGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1578	100.0	283	4	Q9Z9S6	Q9Z9S6 homo sapien
2	1575	99.8	283	4	Q9UM65	Q9UM65 homo sapien
3	1303.5	82.6	283	6	Q9XSZ8	Q9XSZ8 cercopithec
4	271.5	17.2	349	14	Q57100	Q57100 monkeypox v
5	269.5	17.1	348	14	Q57277	Q57277 monkeypox v
6	269.5	17.1	348	14	Q57108	Q57108 monkeypox v
7	269.5	17.1	349	14	Q57291	Q57291 monkeypox v
8	269.5	17.1	349	14	Q57101	Q57101 monkeypox v
9	269.5	17.1	349	14	Q57102	Q57102 monkeypox v
10	266.5	16.9	349	14	Q57284	Q57284 camelpox v
11	266.5	16.9	349	14	Q57098	Q57098 camelpox v
12	265.5	16.8	348	14	Q57103	Q57103 monkeypox v
13	265.5	16.8	349	14	Q57099	Q57099 monkeypox v
14	262.5	16.6	349	14	Q57097	Q57097 camelpox v
15	259	16.4	349	14	Q57111	Q57111 variola v
16	259	16.4	439	4	Q16042	Q16042 homo sapien
17	257.5	16.3	348	14	Q57112	Q57112 variola v
18	257.5	16.3	348	14	Q85407	Q85407 variola v
19	257.5	16.3	351	14	Q57117	Q57117 cowpox viru

20	257	16.3	349	14	057110	057110	variola	vitr
21	257	16.3	349	14	089118	089118	variola	vitr
22	257	16.3	349	14	089098	089098	variola	vitr
23	249	15.8	349	14	057109	057109	variola	vitr
24	246	15.6	300	4	095407	095407	homo	saplen
25	243.5	15.4	351	14	073559	073559	cowpox	vitrur
26	239	15.1	350	14	057116	057116	cowpox	vitrur
27	236.5	15.0	351	14	057121	057121	cowpox	vitrur
28	232.5	14.7	349	14	057305	057305	cowpox	vitrur
29	229.5	14.5	326	14	057122	057122	cowpox	vitrur
30	229	14.5	347	14	057119	057119	cowpox	vitrur
31	228.5	14.5	360	14	057120	057120	cowpox	vitrur
32	228	14.4	326	14	057118	057118	cowpox	vitrur
33	226.5	14.4	350	14	057123	057123	cowpox	vitrur
34	225.5	14.3	347	14	057115	057115	cowpox	vitrur
35	225.5	14.3	355	14	085508	085508	cowpox	vitrur
36	219.5	13.9	267	6	002764	002764	oryctolagus	
37	219.5	13.9	319	6	09TWV9	09TWV9	oryctolagus	
38	218	13.8	320	6	09XS29	09XS29	oryctolagus	
39	215.5	13.7	263	6	09X560	09X560	oryctolagus	
40	213.5	13.5	320	14	057079	057079	cowpox	vitrur
41	213.5	13.5	417	11	09Z0W1	09Z0W1	mus	musculu
42	212.5	13.5	459	11	062327	062327	mus	musculu
43	212	13.4	320	14	057091	057091	ectromelia	
44	212	13.4	320	14	057300	057300	ectromelia	
45	210	13.3	372	4	Q9UHP4	Q9UHP4	homo	saplen

ALIGNMENTS

RESULT	1	
0929356		
ID	Q929356	PRELIMINARY; PRT; 283 AA.
AC	Q929356;	
DT	01-FEB-1997 (TREMBLrel. 02, Created)	
DT	01-JUL-1997 (TREMBLrel. 04, last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)	
DE	HERPESVIRUS ENTRY MEDIATOR.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX	NCBI_TaxId=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=97053782; PubMed=8698196;	
RA	Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;	
RT	"Herpes simplex virus-1 entry into cells mediated by a novel member of	
RL	the TNF/NGF receptor family.";	
Cell	87;427-436(1996)."	
DR	EMBL; U70321; AAB58354.1; -	
DR	HSSP; P25942; 1CDP.	
DR	INTERPRO; IPR001368; -	
DR	PFAM; PF000020; TNFR_C6; 3.	
DR	PROSITE; PS00652; TNFR_NF1; UNKNOWN_1.	
DR	PROSITE; PS50050; TNFR_NF2; 2.	
DR	PRODOM; PD000771; -, 1.	
QO	SEQUENCE 283 AA: 30420 MW; DFCEL46E024F4B CRC64;	

	Query Match	100.0%	Score 1578:	DB 4:	Length 283:
	Best Local Similarity	100.0%	Pred. NO.	2e-143:	
	Matches 283:	Conservative	0:	Mismatches	0:
				Indels	0:
				Gaps	0:
OY	1	MEPPDGMPPMRSPRRIDVLRVLTYLTFNLGAPCAPALPSCKEDEYPVGSECCPKCSFG	60		
Dd	1	MEPPDGMPPMRSTPRIDVLRVLTYLTFNLGAPCAPALPSCKEDEYPVGSECCPKCSFG	60		
OY	61	YRVKACGEITGVCEPCPPGTGYIAHLNGLSKLCOCOMCDPMAGIRASNCRTENAVYG	120		
Dd	61	YRVKACGEITGVCEPCPPGTGYIAHLNGLSKLCOCOMCDPMAGIRASNCRTENAVYG	120		
OY	121	CSPGHCFIVDDGDHCACARAYATSSPGRVRVKGTGESODTLQCNCPGTFSFNGLTLEECQ	180		

```

Db 121 CSPGHCIYVDGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGRTSPNGTLEECQ 180
    |||
QY 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIVTCVGLICVKKRRKRGDVVKVIVS 240
    |||
Db 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIVTCVGLICVKKRRKRGDVVKVIVS 240
    |||
QY 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
    |||
Db 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
    |||

RESULT 2
Q9DM65 PRELIMINARY; PRT; 283 AA.
ID 09DM65
AC 09DM65;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR-LIKE GENE 2 (CD40-LIKE PROTEIN
DE PRECUSOR).
GN TR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kwon B.S., Tan K.B., Ni J.;
RT "A newly-identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation."
RN Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01232; AAD00505.1;
DR EMBL; AF153978; AAF75588.1;
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368;
DR PFAM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 283 AA; 30392 MW; 46CF13C2C70242C1 CRC64;

Query Match 99.8%; Score 1575; DB 4; Length 283;
Best Local Similarity 99.6%; Pred. No. 3.9e-143;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPPMRSTPTDVLRLVLTFLGACVAPALPSCKEDEYVPGSECCPRKSPG 60
    |||
Db 1 MEPPGDMGPPPMRSTPTDVLRLVLTFLGACVAPALPSCKEDEYVPGSECCPRKSPG 60
    |||
QY 61 YRVKEAGELTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
    |||
Db 61 YRVKEAGELTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
    |||
QY 121 CSGHFCIYVDGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGRTSPNGTLEECQ 180
    |||
Db 121 CSGHFCIYVDGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGRTSPNGTLEECQ 180
    |||
QY 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIVTCVGLICVKKRRKRGDVVKVIVS 240
    |||
Db 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIVTCVGLICVKKRRKRGDVVKVIVS 240
    |||
QY 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
    |||
Db 241 VQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
    |||

```

```

RESULT 3
Q9XS28 PRELIMINARY; PRT; 283 AA.
ID 09XS28
AC 09XS28;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE HVEAS.
GN HVEAS.
OS Cercopithecus aethiops (Green monkey) (Griwet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-KIDNEY;
RX MEDLINE=99296730; PubMed=10366573;
RA Foster T.P., Chouliemko V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein."
RL Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1;
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368;
DR PFAM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 82.6%; Score 1303.5; DB 6; Length 283;
Best Local Similarity 82.0%; Pred. No. 4.1e-117;
Matches 232; Conservative 18; Mismatches 30; Indels 3; Gaps 2;
QY 1 MEPPGDMGPPPMRSTPTDVLRLVLTFLGACVAPALPSCKEDEYVPGSECCPRKSPG 60
    |||
Db 1 MEPPGDMGPPPMRSTPTDVLRLVLTFLGSSCYAPALPSCKEDEYVPGSECCPRKSPG 60
    |||
QY 61 YRVKEAGELTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
    |||
Db 61 FHVROACGEQGTGVCEPCPGTYIAHLNGLSKLQCOMCDPAGLRSRNCSTENAVCG 120
    |||
QY 121 CSGHFCIYVDGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGRTSPNGTLEECQ 180
    |||
Db 121 CSGHFCIYVDGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGRTSPNGTLEECQ 180
    |||
QY 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIVTCVGLICVKKRRKRGDVVKVIVS 240
    |||
Db 181 HQTCKSWLTKAGAGTSSSHWMMFLSGSLVIVTCVGLICVKKRRKRGDVVKVIVS 240
    |||
QY 238 IVSVQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 280
    |||
Db 241 IVSVQRRKQAEAGEATVIALQAPPDVTVAVEETIPSTFGSRPNH 283
    |||

```

```

RESULT 4
ID 057100 PRELIMINARY; PRT; 349 AA.
AC 057100;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIGERIA-1971 (71-0082);

```

RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87844; AAB94361.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_c6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SO SEQUENCE 349 AA; 38239 MW; DE6C280D478F2422 CRC64;

Query Match 17.1%; Score 271.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 3.9e-18;
 Matches 59; Conservative 23; Mismatches 80; Indels 19; Gaps 5;

OY 21 LRLVLYLFLGAPC-----YAPALPCKDEYVSGECCPKSPGYRVEACGEL 70
 DB 1 MRSVLYSYILFLSCIINGRDIAPHAPNGCKDKNEYSRNLCLCLCPPTGYASRLCDISK 60
 OY 71 TGVCEPCPPGTIYAHNGLSKCLCO-MCDPAMGLRASRCSTENAVCGSPGHPCIV 129
 DB 61 TNNCTCGSGDTFTSHNNHQAACLSGCRCD--SNQVETRSNCNTHNRICGSPGYICL 118
 OY 130 QGDHCAACRAVATSSPGQRYOKGTESQDTLCONCPPTGTFSPNGTLEECQHQTCSWLV 189
 DB 119 KGSGGCRCTCKTKGIGYGV-SGYTSTGDIVICSPCGGTYS-----HTVSTDKCEPV 172
 OY 190 T 190
 DB 173 T 173

RESULT 5
 O57277 PRELIMINARY; PRT; 348 AA.
 AC O57277;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Zaire-1996(96-17), Zaire-1996 (96-16);
 RL Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88543; AAB94378.1; -
 DR EMBL: U87841; AAB94358.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_c6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SO SEQUENCE 348 AA; 38212 MW; 54019521556C2DBF CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 348;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;

OY 21 LRLVLYLFLGAPC-----YAPALPCKDEYVSGECCPKSPGYRVEACGEL 70
 DB 1 MRSVLYSYILFLSCIINGRDIAPHAPNGCKDKNEYSRNLCLCLCPPTGYASRLCDISK 60
 OY 71 TGVCEPCPPGTIYAHNGLSKCLCO-MCDPAMGLRASRCSTENAVCGSPGHPCIV 129
 DB 61 TNNCTCGSGDTFTSHNNHQAACLSGCRCD--SNQVETRSNCNTHNRICGSPGYICL 118

OY 130 QGDHCAACRAVATSSPGQRYOKGTESQDTLCONCPPTGTFSPN-GTLEECQHQT 183
 DB 119 KGSGGCRCTCKTKGIGYGV-SGYTSTGDIVICSPCGGTYSHTVSTDKCEPV 172

RESULT 6
 O57108 PRELIMINARY; PRT; 348 AA.
 ID O57108;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Zaire-1970 (CONGO-8);
 RL Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88142; AAB94367.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PRAM: PF00020; TNFR_c6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SO SEQUENCE 348 AA; 38212 MW; E55979057DEC91F CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 348;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;

OY 21 LRLVLYLFLGAPC-----YAPALPCKDEYVSGECCPKSPGYRVEACGEL 70
 DB 1 MRSVLYSYILFLSCIINGRDIAPHAPNGCKDKNEYSRNLCLCLCPPTGYASRLCDISK 60
 OY 71 TGVCEPCPPGTIYAHNGLSKCLCO-MCDPAMGLRASRCSTENAVCGSPGHPCIV 129
 DB 61 TNNCTCGSGDTFTSHNNHQAACLSGCRCD--SNQVETRSNCNTHNRICGSPGYICL 118
 OY 130 QGDHCAACRAVATSSPGQRYOKGTESQDTLCONCPPTGTFSPN-GTLEECQHQT 183
 DB 119 KGSGGCRCTCKTKGIGYGV-SGYTSTGDIVICSPCGGTYSHTVSTDKCEPV 172

RESULT 7
 O57291 PRELIMINARY; PRT; 349 AA.
 ID O57291;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RL Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88144; AAB94369.1; -
 DR EMBL: U87842; AAB94359.1; -
 DR EMBL: U8794; AAB94365.1; -
 DR EMBL: U8795; AAB94366.1; -

DR EMBL: U08143; AAB94368.1; -
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38295 MW; CBD2C949ED2B8E7C CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYTFGLGAPC-----YAPALPSCKEDEYVPGSECCPKSPGYRKVEAGGEL 70
 DB 1 MRSVLYSYILFLSCIIINGNDIAPHASNGCKDNEYSRNLLCCLCPPGTIVASRLCDISK 60
 QY 71 TGVYCEPCPGTYIAHLNGLSKLCLOCO-MCDPAMGLRASHNCSTENAVAGCSPGHFCIV 129
 DB 61 TMTQCTPCGSDTFTSHNNHQAQLSCNGRCD--SNQVETRSCTNTHNRICECSPGYCYCL 118
 QY 130 QDDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQHOTKCSMLV 189
 DB 119 KGASGCRCTISKTKGIGYGV-SGYTSTGDIVICSPCGPGTYS-----HTVSTDKCEPVV 172
 QY 190 T 190
 DB 173 T 173

RESULT 8
 ID 057101 PRELIMINARY; PRT; 349 AA.
 AC 057101;

DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.

OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_Taxid=10244;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZAIRE-1977 (77-0666);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U08143; AAB94362.1; -
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38311 MW; 02F65B00CEB858BE CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYTFGLGAPC-----YAPALPSCKEDEYVPGSECCPKSPGYRKVEAGGEL 70
 DB 1 MRSVLYSYILFLSCIIINGNDIAPHASNGCKDNEYSRNLLCCLCPPGTIVASRLCDISK 60
 QY 71 TGVYCEPCPGTYIAHLNGLSKLCLOCO-MCDPAMGLRASHNCSTENAVAGCSPGHFCIV 129
 DB 61 TMTQCTPCGSDTFTSHNNHQAQLSCNGRCD--SNQVETRSCTNTHNRICECSPGYCYCL 118
 QY 130 QDDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQHOTKCSMLV 189

DB 119 KGASGCRCTISKTKGIGYGV-SGYTSTGDIVICSPCGPGTYS-----HTVSTDKCEPVV 172
 QY 190 T 190
 DB 173 T 173

RESULT 9
 ID 057102 PRELIMINARY; PRT; 349 AA.
 AC 057102;

DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.

OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_Taxid=10244;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BENIN-1978 (78-3945);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U08146; AAB94363.1; -
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match 17.1%; Score 269.5; DB 14; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6e-18;
 Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYTFGLGAPC-----YAPALPSCKEDEYVPGSECCPKSPGYRKVEAGGEL 70
 DB 1 MRSVLYSYILFLSCIIINGNDIAPHASNGCKDNEYSRNLLCCLCPPGTIVASRLCDISK 60
 QY 71 TGVYCEPCPGTYIAHLNGLSKLCLOCO-MCDPAMGLRASHNCSTENAVAGCSPGHFCIV 129
 DB 61 TMTQCTPCGSDTFTSHNNHQAQLSCNGRCD--SNQVETRSCTNTHNRICECSPGYCYCL 118
 QY 130 QDDDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQHOTKCSMLV 189
 DB 119 KGASGCRCTISKTKGIGYGV-SGYTSTGDIVICSPCGPGTYS-----HTVSTDKCEPVV 172
 QY 190 T 190
 DB 173 T 173

RESULT 10
 ID 057284 PRELIMINARY; PRT; 349 AA.
 AC 057284;

DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.

OS Camelipox virus (strain CP-1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_Taxid=28873;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-DUBAI-1992 (CP-5), SOMALIA-1978;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;

Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87840; AAB94357.1; -
 DR EMBL: U87837; AAB94354.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF000020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38036 MW; EA412AE86E090E4 CRC64;

Query Match 16.9%; Score 266.5; DB 14; Length 349;
 Best Local Similarity 33.1%; Pred. No. 1.2e-17;
 Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

OY 21 LRLVLYLFLAPC-----YAPALPSCKEDEYVSGCCPKSPGYRVKACGEL 70.
 DB 1 MKSVLYSTILSLCIIINGRDVTPAPNSGCKDNEYRHNLCCLSCPPGYASRLCDISK 60
 OY 71 TGVCEPCPGTYIAHLNGLSKLCQO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
 DB 61 TINTQCTPGSGFTFSRNNHLPACLSGNGRCD--SNQVETRSCNTHNHRICSGSGYICIL 118
 OY 130 QDGDHCACRAVATSSPGQRYOKGTESDPTLCNCPGTFSPN-GTLEECQ 180
 DB 119 KSSGCKACVSGTCKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCE 169

RESULT 11

ID 057098 PRELIMINARY; PRT; 349 AA.

AC 057098;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Camelpox virus (strain CP-1).
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=28873;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SAUDI-M3;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87839; AAB94356.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF000020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 37978 MW; 8630FEAED7A584B5 CRC64;

Query Match 16.9%; Score 266.5; DB 14; Length 349;
 Best Local Similarity 33.1%; Pred. No. 1.2e-17;
 Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

OY 21 LRLVLYLFLAPC-----YAPALPSCKEDEYVSGCCPKSPGYRVKACGEL 70
 DB 1 MKSVLYSTILSLCIIINGRDVTPAPNSGCKDNEYRHNLCCLSCPPGYASRLCDISK 60
 OY 71 TGVCEPCPGTYIAHLNGLSKLCQO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
 DB 61 TINTQCTPGSGFTFSRNNHLPACLSGNGRCD--SNQVETRSCNTHNHRICSGSGYICIL 118
 OY 130 QDGDHCACRAVATSSPGQRYOKGTESDPTLCNCPGTFSPN-GTLEECQ 180
 DB 119 KSSGCKACVSGTCKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCE 169

RESULT 12

ID 057103 PRELIMINARY; PRT; 348 AA.

AC 057103;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZAIRE-1979 (79-0005);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87847; AAB94364.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF000020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 348 AA; 38184 MW; 34A5E68B27907B5 CRC64;

Query Match 16.8%; Score 265.5; DB 14; Length 348;
 Best Local Similarity 32.0%; Pred. No. 1.4e-17;
 Matches 56; Conservative 25; Mismatches 79; Indels 15; Gaps 5;

OY 21 LRLVLYLFLAPC-----YAPALPSCKEDEYVSGCCPKSPGYRVKACGEL 70
 DB 1 MKSVLYSTILSLCIIINGRDVTPAPNSGCKDNEYRHNLCCLSCPPGYASRLCDISK 60
 OY 71 TGVCEPCPGTYIAHLNGLSKLCQO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
 DB 61 TINTQCTPGSGFTFSRNNHLPACLSGNGRCD--SNQVETRSCNTHNHRICSGSGYICIL 118
 OY 130 QDGDHCACRAVATSSPGQRYOKGTESDPTLCNCPGTFSPN-GTLEECQ 183
 DB 119 KSSGCKACVSGTCKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCE 172

RESULT 13

ID 057099 PRELIMINARY; PRT; 349 AA.

AC 057099;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-STERRA LEONE-1970 (70-0266);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87843; AAB94360.1; -
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF000020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 SQ SEQUENCE 349 AA; 38321 MW; FE449028C933F57 CRC64;

```

Query Match          16.8%; Score 265.5; DB 14; Length 349;
Best Local Similarity 32.6%; Pred. No. 1.4e-17;
Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYITFLGAPC-----YAPALPSCKEDEYVPGSECCPKSPGYRVKACGEL 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRSVLYSYILFLSCIINGRDIAHPAPNGKCKDNEYSRNLCCSCPPGTIVASRLCDK 60

QY 71 TGYVCEPCPGPTIYIAHLNGLSKLQCO-MCDPAMGLASRNCSTENAVCGSPGHFCIV 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TMTCTCGSGTFTSHNNHLPACLSGNCRCN--SNQVETRSCHNTJHNRICCSPGYICLL 118

QY 130 QDGDHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECOHQTKCSMLV 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 KGALGCRICISKTGCGIGYV-SGITSAGDVICSPCGGTTT-----HTVSTDKCEPV 172

QY 190 T 190
Db 173 T 173

RESULT 14
057097 ID 057097 PRELIMINARY; PRT; 349 AA.
AC 057097;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE TMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Camelox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=28873;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=IRAN (CP-1);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U87838; AAB94355.1; -.
DR HSSP: P25942; ICDF.
DR INTERPRO: IPR001368; -.
DR PFAM: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PRODOM: PD000771; -.
SQ SEQUENCE 349 AA; 37944 MW; 829EA54EDAC60455 CRC64;

Query Match          16.6%; Score 262.5; DB 14; Length 349;
Best Local Similarity 33.1%; Pred. NO. 2.8e-17;
Matches 57; Conservative 23; Mismatches 77; Indels 15; Gaps 5;

QY 21 LRLVLYITFLGAPC-----YAPALPSCKEDEYVPGSECCPKSPGYRVKACGEL 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRSVLYSYILFLSCIINGRDVTPYAPSNCKKDNFKRHHLLCCLSCPPTIVASRLCDK 60

QY 71 TGYVCEPCPGPTIYIAHLNGLSKLQCO-MCDPAMGLASRNCSTENAVCGSPGHFCIV 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TMTCTCGSGTFTSRNNHLPACLSGNCRCN--SNQVETRSCHNTJHNRICCSPGYICLL 118

QY 130 QDGDHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECOHQTKCSMLV 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 KGSSGCAKACVQTKGIGYV-SGHTSAGDVICSPCGIGTYSRTVSSADKCE 169

RESULT 15
057111 ID 057111 PRELIMINARY; PRT; 349 AA.
AC 057111;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)

```

```

DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE TMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MINOR, STERRA LEONE-1968 (SLN-68);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U88150; AAB94375.1; -.
DR HSSP: P25942; ICDF.
DR INTERPRO: IPR001368; -.
DR PFAM: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PRODOM: PD000771; -.
SQ SEQUENCE 349 AA; 38209 MW; 3D22ED1F15329942 CRC64;

Query Match          16.4%; Score 259; DB 14; Length 349;
Best Local Similarity 28.5%; Pred. NO. 6.1e-17;
Matches 67; Conservative 25; Mismatches 101; Indels 42; Gaps 8;

QY 21 LRLVLYITFLGAPC-----YAPALPSCKEDEYVPGSECCPKSPGYRVKACGEL 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRSVLYSYILFLSCIINGDAPAYTPNGKCKDTEYKRHHLLCCLSCPPTIVASRLCDK 60

QY 71 TGYVCEPCPGPTIYIAHLNGLSKLQCO-MCDPAMGLASRNCSTENAVCGSPGHFCIV 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TMTCTCGSGTFTSRNNHLPACLSGNCRCN--SNQVETRSCHNTJHNRICCSPGYICLL 118

QY 130 QDGDHCACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECOHQTKCSMLV 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 KGSSGCAKACVQTKGIGYV-SGHTSVGDVICSPCGFGTYSVSTDKCEPVNNTFN 177

QY 178 ECQ-----HOKKCSMLYTKAGAGTSSSHWMMFLSGSLVIVICSTYGLIIC 224
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 YIDVEITLYPVNDTSCHRTT---TGLSES-----ILTSELTITMHHNDCNPVC 224

```

Search completed: April 25, 2001, 17:36:02
Job time: 108 sec

THIS PAGE BLANK (USPTO)

Db 61 YRVKACGELTGTCEPCPGTYIAHLNGLSKLCQCMCPAMGLRATRNCSRTENAVCG 120
QY 121 CSPHFCIVDDGHCACRAVATSSPGORVOKGTESDPTLCCPCPGTSPNLTLECCQ 180
Db 121 CSPHFCIVDDGHCACRAVATSSPGORVOKGTESDPTLCCPCPGTSPNLTLECCQ 180
QY 181 HQTCSWLVYKAGAGTSSSHWMMFLSGSLVIVVSTVGLITCVRKRRRGDVVKKYVS 240
Db 181 HQTCSWLVYKAGAGTSSSHWMMFLSGSLVIVVSTVGLITCVRKRRRGDVVKKYVS 240
QY 241 VORRKEABEBAIVIALQAPPDVTVAVEETIPSTGRSPNH 283
Db 241 VORRKEABEBAIVIALQAPPDVTVAVEETIPSTGRSPNH 283
RESULT 2
US-09-042-785A-11
; Sequence 11, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-042-785A-11
Query Match 17.5%; Score 276.5; DB 4; Length 289;
Best Local Similarity 27.9%; Pred. No. 1.9e-17;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;

Db 142 VCHPCPVGFSSNQSLFEKCYPWTSCEDKNMLEYLQK---GTSQTNVYIGLKSRRALVY 198
QY 216 CSTVGLITC-----VKR--RRRGDVVAVIVSVQRRKEABEBAIVIALQAPPDVT 266
Db 199 PVWGLITTFGVFLYIKVYKRRPKDN--EMLPPAARRQDPQEME-----DYPGHNTA 249
QY 267 VAVEETI 273
Db 250 APVQETL 256
RESULT 3
US-09-042-785A-10
; Sequence 10, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-042-785A-10
Query Match 17.0%; Score 267.5; DB 4; Length 277;
Best Local Similarity 26.1%; Pred. No. 1.2e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

Db 176 Q-AGTNTDVCQPDRLALVPIIFGLFA-----ILLVLFYKAKKPKLNK 225
QY 252 AFVTEALQAPPDV-----TTVAVEETI 273
Db 226 AP--HPKQEPQEIHFPPDLPGSNAAAPVQETL 255

RESULT 4
US-08-974-022-47
; Sequence 47, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Denavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-47

Query Match 16.5%; Score 260; DB 3; Length 207;
Best Local Similarity 31.5%; Pred. No. 3.8e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;
QY 20 VLRLVLYLTLGAPCYALP-----SCKEDYPVGSSECCPKSPGYRVKACGELTGT 73
Db 1 MLRLIALLCV-VVYGDVDPYSSNCGKHDEKDLCCASHCPFYASRLCGPSNT 59
QY 74 VCEPCPGTYIAHNGSKLCCQMDPAMG-LRASRNCSTENAVCGSGPHFCIVODG 132
Db 60 VCSPEDEGTFTASTNHAAPACVSCR--GPGTGHLSQPCDTHDVCNCSGTGNYCLKGQ 117
QY 133 DHCACRAVATSSPGQVVGKGTESODTLCCNCPGTFSPN-GTLEEC----- 179
Db 118 NGCRIC-APQTKCPAGVSGHTRAGDTLCEKCPHTYSLSLSTFKCGTSFNITSVGFN 176
QY 180 ---OHQTKCSMLVTKAG 193
Db 177 LYPVNETSCT---TTAG 190

RESULT 5
US-08-292-549-2

; Sequence 2, Application US/08292549
; Patent No. 5464938
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,549
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,330
; FILING DATE: 10/19/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2602-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-292-549-2

Query Match 16.5%; Score 260; DB 1; Length 325;
Best Local Similarity 31.5%; Pred. No. 6.6e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;
QY 20 VLRLVLYLTLGAPCYALP-----SCKEDYPVGSSECCPKSPGYRVKACGELTGT 73
Db 1 MLRLIALLCV-VVYGDVDPYSSNCGKHDEKDLCCASHCPFYASRLCGPSNT 59
QY 74 VCEPCPGTYIAHNGSKLCCQMDPAMG-LRASRNCSTENAVCGSGPHFCIVODG 132
Db 60 VCSPEDEGTFTASTNHAAPACVSCR--GPGTGHLSQPCDTHDVCNCSGTGNYCLKGQ 117
QY 133 DHCACRAVATSSPGQVVGKGTESODTLCCNCPGTFSPN-GTLEEC----- 179
Db 118 NGCRIC-APQTKCPAGVSGHTRAGDTLCEKCPHTYSLSLSTFKCGTSFNITSVGFN 176
QY 180 ---OHQTKCSMLVTKAG 193
Db 177 LYPVNETSCT---TTAG 190

RESULT 6
US-09-042-785A-9
; Sequence 9, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-9

Query Match 16.5%; Score 260; DB 4; Length 325;
Best Local Similarity 31.5%; Pred. No. 6.6e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLTFLGACVAPALP-----SKDEVPVSECCPKSPGRVKEAGGELTGT 73
DB 1 MLRLIALVCV-VVYGDVPPYSSNOGCGHDEKDLCCASCHPGFYASRLCGPSNT 59
QY 74 VCEPCPGTGYIAHLNGLSKLQCMCDPAMG-LRASRNCSTENAVCGSPGHFCIVODG 132
DB 60 VCSPEDEGFTFASNNHAPACVSCR--GPCGHLSESGPCDRTHRVNCSTGNVCLLKQ 117
QY 133 DHCACRAVATSSPGQRYOKGTESDTLQNCPPGTFSPN-GTLEEC-----179
DB 118 NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPHTYSDSLPTERCSTSFNYISVGFN 176
QY 180 ---QHOKCSMLVTKAG 193
DB 177 LYPVNETSCT---TTAG 190

RESULT 7
PCT-US91-02207-2
Sequence 2, Application PC/TUS9102207
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02207
FILING DATE: 19910329
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02207-2

Query Match 16.5%; Score 260; DB 5; Length 325;
Best Local Similarity 31.5%; Pred. No. 6.6e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLTFLGACVAPALP-----SKDEVPVSECCPKSPGRVKEAGGELTGT 73
DB 1 MLRLIALVCV-VVYGDVPPYSSNOGCGHDEKDLCCASCHPGFYASRLCGPSNT 59
QY 74 VCEPCPGTGYIAHLNGLSKLQCMCDPAMG-LRASRNCSTENAVCGSPGHFCIVODG 132
DB 60 VCSPEDEGFTFASNNHAPACVSCR--GPCGHLSESGPCDRTHRVNCSTGNVCLLKQ 117
QY 133 DHCACRAVATSSPGQRYOKGTESDTLQNCPPGTFSPN-GTLEEC-----179
DB 118 NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPHTYSDSLPTERCSTSFNYISVGFN 176
QY 180 ---QHOKCSMLVTKAG 193
DB 177 LYPVNETSCT---TTAG 190

RESULT 8
US-08-974-022-48
Sequence 48, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
City: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:

```

? ATTORNEY/AGENT INFORMATION:
? NAME: Winters, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 227 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? OS-08-974-022-48

```

Query Match	16.4%	Score 259	DB 3:	length 227
Best Local Similarity	32.8%	Pred. No.	5.3e-16	
Matches	59	Conservative	23	Mismatches 76; Indels 22; Gaps 6

```

QY 92 KCLTCCOMCDPMAGIRASNN-----GSRTEANVAGCGSPGHCIIVODSDHCACCAVATSS 145
Db 92 ECLSC-----GSRCSDDVETGACIRREDNRRIOTCRPMWCAHLSKRGEGRLCAPLKKCR 144
QY 146 PGQRYQKGGTSSQTLTLCNCPRTGFS-PNGTLEECQIQTKCSMLVYTAAG-----TSSS 1399
Db 145 PGEVGARGTSTISVYCKPCPCAGFTSNSTSDTLCRPHQICNVAALPDGNSRDVATVTS 204

```

Query March	16.4%;	Score 259;	DB 1;	Length 461;
Best Local Similarity	32.8%;	Pred. No. 1.2e-15;		
Matches 59;	Conservative 23;	Mismatches 76;	Indels 22;	Gaps 6;

QY	35	YAPALPLS-CKEDEV--PVGSECCPKSCPGYRVKKAAGELGTGTVECPCPGTYIAHNLGIS	91
Db	32	YAPGEGSTCRLEREYDYQFAOMCCSCPGNAHKAVFCTRTSDVDCSCDESTYOLMNPV	91
QY	92	KCLQCOMCDPAMGLASRN-----CSTRENAVGCCSGHCTIYDDGDHCACRAVATSS	145
Db	92	ECLISC-----GSRCSDDOYETQACTREONNICTCRGQWYALSKQECRCRLCAPLRKR	144
QY	146	PGQROKRGSTESODPLCNCPGTFRS-ENGTLSEEOHQTCKSMLYTKAGAG-----TSSS	199
Db	145	PGFGVARGTETSDVYCCAPCAAGTISNTTSSDLCRPHQICNVVAIPGNAAMDVACTTSS	204

```

RESULT 10
US-08-650-000-2
Sequence 2, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors

```

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

RESULT 10
 US-08-650-000-2
 Sequence 2, Application US/08650000
 Patent No. 5945397
 GENERAL INFORMATION:
 APPLICANT: Smith, Craig A.
 APPLICANT: Goodwin, Raymond G.
 APPLICANT: Beckmann, M. Patricia
 TITLE OF INVENTION: Tumor Necrosis Factor Receptors
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immune Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/650,000
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,453
 FILING DATE:
 APPLICATION NUMBER: US/08/038,765
 FILING DATE:
 APPLICATION NUMBER: US 403,241
 FILING DATE: 05-SEP-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 405,370
 FILING DATE: 11-SEP-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 421,417
 FILING DATE: 13-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 523,635
 FILING DATE: 10-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Wight, Christopher L.
 REGISTRATION NUMBER: 31,680
 REFERENCE/DOCKET NUMBER: 2501-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 461 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 17:31:39 ; Search time 13.01 Seconds
(without alignments)
1494.896 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 1578
Sequence: 1 MEPPGDMGPPMRSTPRIDV.....VTVAVETIPSTGSRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276.5	17.5	305	2 A46476	B cell-associated
2	267.5	17.0	277	2 A60771	T2 protein - rabd1
3	260	16.5	325	2 B43692	tumor necrosis fac
4	259	16.4	461	1 A35356	hypothetical prote
5	257.5	16.3	348	2 T28623	G2R protein - Vari
6	257	16.3	349	2 D72175	gene G4R protein -
7	257	16.3	349	2 D36858	tumor necrosis fac
8	253	16.0	435	2 T54182	tumor necrosis fac
9	240.5	15.2	271	2 S12783	OX40 antigen precu
10	238.5	15.1	326	1 GQVZML	T2 protein - myxom
11	215.5	13.7	272	2 I48700	gene oxa40 protein
12	213.5	13.5	474	2 B38634	tumor necrosis fac
13	212.5	13.5	459	2 I48854	gene murine tumour
14	206.5	13.1	324	2 JC2395	Fas antigen precu
15	206	13.1	335	2 A40036	apoptosis-mediatin
16	205	13.0	327	2 A46484	apoptosis-mediatin
17	203.5	12.9	425	1 A26431	nerve growth facto
18	198.5	12.6	416	1 JN0006	nerve growth facto
19	194.5	12.3	277	2 I37552	OX40 homolog - hum
20	192	12.2	461	1 GQRTT1	tumor necrosis fac
21	190	12.0	427	1 GQHUN	nerve growth facto
22	186	11.8	314	2 I37383	FAS soluble protei
23	176.5	11.2	256	2 B32393	tumor necrosis fac
24	172.5	10.9	461	2 JC4302	tumor necrosis fac
25	171	10.8	250	1 A49053	CD27 antigen precu
26	168.5	10.7	454	1 GQWST1	tumor necrosis fac
27	161	10.2	255	2 I38426	lymphocyte activat
28	159	10.1	255	2 A42086	CD30 antigen precu
29	155	9.8	455	1 GQHOT1	tumor necrosis fac

30	148	9.4	260	1 A46517	CD27 antigen precu
31	144.5	9.2	493	2 JC5486	membrane glycoprot
32	143.5	9.1	1786	1 MMHUB1	laminin beta-1 cha
33	139.5	8.8	5376	2 T42215	zonadhesin - mouse
34	135.5	8.6	1274	2 T42017	cysteine rich prot
35	135	8.6	1574	2 T13954	MEGF6 protein - ra
36	134	8.5	2824	2 T22759	hypothetical prote
37	133.5	8.5	4391	2 A38096	perlecan precursor
38	130.5	8.3	1786	1 MMMSB1	laminin beta-1 cha
39	128.5	8.1	2533	2 T28675	alpha-51D immobill
40	128.5	8.1	2533	2 T28674	alpha-51D-immobill
41	127.5	8.1	596	2 A45664	variant-specific s
42	127.5	8.1	1372	2 T25933	hypothetical prote
43	127.5	8.0	3707	2 S18252	heparan sulfate pr
44	127	8.0	1797	2 A55677	laminin beta-2 cha
45	127	8.0	1798	2 S53869	laminin beta-2 cha

ALIGNMENTS

RESULT 1

A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A>Title: Differential Increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1305 <TOR>
A:Cross-references: GB:M83312; NID:g1553058
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
A:Note: this translation is not annotated in GenBank entry M83312, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockey
J. Immunol. 149, 3921-3926, 1992
A>Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1287, 'LV' <GR>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A:Experimental source: BALB/c, liver
A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match	17.5%	Score 276.5;	DB 2;	Length 305;
Best Local Similarity	27.9%	Pred. NO. 2.5e-13;		
Matches 69;	Conservative 43;	Mismatches 106;	Indels 29;	Gaps 8;
QY	41	SCKEDEYVPSSECCPKSPGYRVKACGELGTVCBPCPGTYIAHNGLSKLCQCMCD	100	
DB	25	TCSGKQYLHDGQCDDQPGSRILSHCTALEKTQCHCDGSGFSAQNNREIRCHQHHCE	84	
QY	101	PAMGLASRNCSTENAVCCSGPHFCIVDGDHCAACRAVANSPPQRYOKGSGSDPT	160	
DB	85	PNQGLRVKKEGTAEVDVCTCKEKGHCTSKD---CEACAOHTPCIPFGVEMAKETETDF	141	
QY	161	ICQNCPRGTSPNCTL-EEOHOKKS---WLVTKAGAGSSSHHWMLFSLVIVV	215	
DB	142	VCHPCPVGFPSNOSSLKECTPMTSCDKMLEVLOK---GISQTNVICGLSKRRRALVI	198	
QY	216	CSTVGLIIC-----VKR--RKPRGDVVRVIVSVQRRROEAGEATVIALQAPDVT	266	

Db 199 PVMGILITIFGVFLYIKKVKKKPKDN--EMLPPAARQDPQENE-----DIPGNHTA 249
 QY 267 VAVEETI 273
 Db 250 APVQETL 256

RESULT 2

A60771
 B-cell activation protein CD40 precursor - human
 N/Alternate names: B-cell surface antigen Bp50
 C/Species: Homo sapiens (hmn)
 C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C/Accession: S04460; A60771
 R/Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBO J. 8, 1403-1410, 1989
 A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A/Reference number: S04460; MUID:89356608
 A/Accession: S04460
 A/Molecule type: mRNA
 A/Residues: 1-277 <STA>
 A/Cross-references: EMBL:X60592; NID:929850; PIDN:CAA3045.1; PID:929851
 R/Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-Lik
 A/Reference number: A60771; MUID:89093941
 A/Accession: A60771
 A/Molecule type: protein
 A/Residues: 21-50 <BRA>
 A/Experimental source: Burkitt lymphoma cell line Raj1
 C/Genetics:
 A/Gene: GDB:CD40
 A/Cross-references: GDB:215268; OMIM:109535
 A/Map position: 20q12-20q13.2
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keyworfams: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:21-193/Domain: extracellular #status predicted <EXT>
 F:194-215/Domain: transmembrane #status predicted <TM>
 F:216-277/Domain: intracellular #status predicted <CY>
 F:153/180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 267.5; DB 2; Length 277;
 Best Local Similarity 26.1%; Pred. No. 1.1e-12;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VLRLVLYLFLGAPCYAPAL-----PSCKEDYPPVSGCCPKSPGYRVKACGELTGV 74
 Db 1 MVRRLPLOCVLWG--CLITAVHPRPTACREKQYLINQCCSLCPGKGLVSDCFEETE 58
 QY 75 CEECPPTGYIAHLNGLSKLCQCCOMPAMG-LRASRNCSTENAVCGSPGHCTIVODGDH 134
 Db 59 CLPCGSEEFIDTMRNRETHQHKKYCDNLGLRVQCKTSETDITCTCEEGWHC---TSEA 115
 QY 135 CACRAATATSPGQRYVKGKTESODTLQCNCPPTFS-PKCTLECHQHKCSM--LYTK 191
 Db 116 CESCVLHRSCTPGFVQKQATGVSDTICEPVGFFSNVSAPEKCHPMTSCETKDLVQ 175
 QY 192 AGATSSSHWMMFLSGSLYIVICSTVGLICVKKRRPGDVKYIVSVQRKQOAGE 251
 Db 176 Q-ACNTKTDVYCGQDRLRALVPIPIFGILFA-----ILLVLFYIKKAKKPTNK 225
 QY 252 ATVTEALQAPPDV-----TTVAVEETI 273
 Db 226 AP--HPKQEPQETINFPDDLPGSNTAAVQETL 255

RESULT 3
 B43692
 T2 protein - rabbit fibroma virus

C/Species: rabbit fibroma virus, Shope fibroma virus
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: B43692
 R/Upton, C.; Delange, A.M.; McPadden, G.
 Virology 160, 20-30, 1987
 A/Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer
 A/Reference number: A43692; MUID:87321103
 A/Accession: B43692
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-325 <UPT>
 A/Cross-references: GB:M17433
 C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F:64-105/Domain: NGF receptor repeat homology <NG>
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 16.5%; Score 260; DB 2; Length 325;
 Best Local Similarity 31.5%; Pred. No. 4.3e-12;
 Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLYLFLGAPCYAPAL-----SCKEDYPPVSGCCPKSPGYRVKACGELTGV 73
 Db 1 MLRLIALVLCV-VVYGDVDPYSSNCGKCGHDEKDLCCASCHPFGYASRLCGPSNT 59
 QY 74 VCECPPTGYIAHLNGLSKLCQCCOMPAMG-LRASRNCSTENAVCGSPGHCTIVODG 132
 Db 60 VCSPECEGTFTASTNNAAPACVSCR--GPTGHLSESPPCPTHDRVCNCTGNYCLLKG 117
 QY 133 DHCACRAVATSSPGQRYVKGKTESODTLQCNCPPTFSN-GLTEBC----- 179
 Db 118 NGCRIC-APQTKCPAGVSGVGHTRAGDTLCEKPPHTYSLSLPTERCGRSFNVISGFN 176
 QY 180 ---QHOKCSMLVTKAG 193
 Db 177 LYPVENISCT--TTAG 190

RESULT 4

A35356
 Tumor necrosis factor receptor 2 precursor [validated] - human
 N/Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
 C/Species: Homo sapiens (hmn)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
 C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I18094
 R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
 A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular A/Reference number: A35356; MUID:90260639
 A/Accession: A35356
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-461 <SML>
 A/Cross-references: GB:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186
 R/Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A/Title: A second tumor necrosis factor receptor gene product can shed a naturally oc A/Reference number: A36475; MUID:91045991
 A/Accession: A36475
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-195, 197-461 <KOH>
 A/Cross-references: GB:M55994; GB:M38549; NID:q339757; PIDN:AAA36755.1; PID:q339758
 R/Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lamm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
 A/Title: Two human TNF receptors have similar extracellular, but distinct intracellular A/Reference number: A48416; MUID:91370690
 A/Accession: A48416
 A/Status: preliminary
 A/Molecule type: mRNA; protein
 A/Residues: 23-461 <DEM>
 A/Cross-references: GB:S63368; NID:q235648; PIDN:AA19824.1; PID:q235649
 A/Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)

```

R.Heller, R.A.Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A>Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140 / 'P', 142-195, 'R', 197-362, 'T', 364-461 <HET>
A:Cross-references: GB:M55857; MID:g339751; PIDN:AA6362.1; PID:g339752
R.Loescher, H.; Schlegel, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A>Title: Purification and partial amino acid sequence analysis of two distinct tumor necr
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>
R.Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A>Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215
A:Accession: B35010
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R.Kuhmert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A>Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: I38094; MUID:95121934
A:Accession: I38094
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
C.Genetics:
A:Gene: GDB:TNFBR2
A:Cross-references: GDB:I25914; OMIM:191191
A:Map position: Ip36.2-Ip36.2
A:Introns: 26/3
A>Note: The list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F.1-12/Domain: signal sequence #status predicted <SIG>
F.23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F.7-107/Domain: NGF receptor repeat homology <NG1>
F.78-119/Domain: NGF receptor repeat homology <NG2>
F.120-142/Domain: NGF receptor repeat homology <NG3>
F.164-201/Domain: NGF receptor repeat homology <NG4>
F.262-279/Domain: transmembrane #status predicted <TMN>
F.280-461/Domain: Intracellular #status predicted <INT>
F.171,193/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match      16.4%; Score 259; DB 1; Length 461;
Best Local Similarity 32.8%; Pred. No. 6.8e-12;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

QY 35 YAPALPS-CKEDEY--PWGSECCPKSCPGYRKVKEAGELTGVCPECPPTGYIAHLNGLS 91
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 32 VAPFGSTCRLEFYLDQDAOMCKSCSPGQAHVCTRTSDPVDCSDCSDDTYITOLMNVF 91
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 92 KCLQCOMCDPAMGLRASRN-----CSRTENAVCGCSFGHCITYODGDHCAACRAYATSS 145
   :|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 92 ECLSC-----GSRCCSDQVETQACTREQNRICTRCRGWCALSKGCRCLCAPLRKCR 144
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 146 PGQRQAKGGTESQDPLQCNCPPGTFS-ENGLIECOHQTKSMVLTVKAGAG-----TSSS 199
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 145 PEGVARPETERSDVVKPCACPGTFSNTTSTDICRPQIIONVVAIPGNASMDAVCTSTS 204
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

[illegible]

```

Oy 178 ECQ-----HOTKCSWLVTKAGAGTSSSHMMWMTLSGSLVIYI 214
Db 178 YIDVEITLTPVNDTSCRTT---TGLSES-----ILTSELITM 214

RESULT 7
D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Description: not shown
A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BL>
A:Cross-references: CB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolymhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, S.M.
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: G4R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.3%; Score 257; DB 2; Length 349;
Best Local Similarity 29.3%; Pred. No. 7.6e-12;
Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;

Oy 21 LRLVLYLFLAPC-----YAPALPSCKEDEIPVSGECCPKSPGTRVKEACGEL 70
Db 1 MKSVLYLILSLCIIINGRDAAPYTPENGCKDTEYKRNHMLCCLSCPGTYASRLDSK 60
Oy 71 TGTVCEPCPPETVIAHLNGLSKLOQ-MCDPANGLRASRNCSSTENAVGCGSPGHFCIV 129
Db 61 TINTQCTPGSGSTFTSRNNHLPACLSGCRGN--SNQYETNSCNTHNRIKTECSPGYICLL 118
Oy 130 QDGHCAACRAVYATSPGQRYVQKGTESODTLCONCPGTFPS-----PNGTLE 177
Db 119 KGSSCCKACVQSQTGCGIGYV-SGHTSYGDVYICSPCGGTSHIVSSADKCEPVPNNFTFN 177
Oy 178 ECQ-----HOTKCSWLVTKAGAGTSSSHMMWMTLSGSLVIYI 214
Db 178 YIDVEITLTPVNDTSCRTT---TGLSES-----ILTSELITM 214

RESULT 8
154182

```

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: U54182
R:Blaes, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A>Title: Construction and evaluation of a hncDNA library of human l2p transcribed seq
A:Reference number: I54182; MUID:93252381
A:Accession: U54182
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
C:Cross-references: GB:L04270; NID:g33976L; PIDN:AAA36757.1; PID:g339762
C:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 16.0%; Score 253; DB 2; Length 435;
Best Local Similarity 26.7%; Pred. No. 1.8e-11;
Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;

Y 4 PG-DWGPPPMWSTPRTDVLRLVLYTLFL-----GAPCVKALPSCK--EDEX--PVGS 51
Db 10 PGLAMGP-----LVLLGLELLASQPOANPVPAISEMOTCRDOEKETFEPOHR 56
Y 52 ECPKSPGYRYKENGCELTGVCEPCPGTYIHLNLKSLCOCMCPMAGLRASNC 111
Db 57 ICGSICPGPTVYSAKCSIRDTVCATCAENSYNEHMYNLITCOLCRCDPVMGLEIAPC 116
Y 112 SRTENAUVGCSPGHFCIVQDGDHACARAYTSSFG-----QRVKGTESQDTLCNC 165
Db 117 TSKRRYTQRCRCPGMFCAM-ALECTHCELLSDCPEGTAEIKDEVGKNNH----CVPC 170
Y 166 PRGPR-----SNGLTLEEQHOTKC-SMLVTKAGAGTSSSHWWMM-----PLSGSLVI 212
Db 171 KAGHFQNTSSPSA---RCOPHTRCENOGLVEAAPTADSDTTCKNNPLELPBMSGTRLM 227
Y 213 VIVGSTVGLII-----CVKRRRPGRDVNVIVSVOKRKROEAEGEATVIALQAP----- 261
Db 228 LAVLLPLAFILLMTVFESCIMKSHP--SLCKKLISLKKRRQGSGPNVAVASWEPRAPH 285
Y 262 --PDVTVAVEETIPSTFTGRSP 281
Db 286 YFPDL---VOPLPLISGDVSP 303

RESULT 9
SI2783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: SI2783; S08036
R:Maliet, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A>Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
A:Reference number: SI2783; MUID:90214614
A:Accession: SI2783
A:Molecule type: mRNA
A:Residues: 1-271 <NAL>
C:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TMW>

Query Match 15.2%; Score 240.5; DB 2; Length 271;
Best Local Similarity 34.9%; Pred. No. 9.9e-11;

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2001, 17:34:34 ; Search time 8.99 Seconds

(without alignments)
1078.343 Million cell updates/sec

Title: US-08-741-095b-26

Percent score: 1578
1 MEPPGDMGPPPMKSTPRTDV.....VTVVAVEETIPSEFTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	276.5	17.5	289 1	CD40_MOUSE
2	267.5	17.0	277 1	CD40_HUMAN
3	267	16.9	269 1	CD40_BOVIN
4	260	16.5	325 1	V72_SEVKA
5	259	16.4	461 1	TNR2_HUMAN
6	257	16.3	349 1	WC22_VARY
7	253	16.0	435 1	TNR2_HUMAN
8	245.5	15.6	415 1	TNR2_MOUSE
9	240.5	15.2	271 1	OX40_RAT
10	238.5	15.1	326 1	V72_MYXVL
11	236	15.0	332 1	FASA_PIG
12	215.5	13.7	272 1	OX40_MOUSE
13	213.5	13.5	474 1	TNR2_MOUSE
14	206.5	13.1	324 1	FASA_RAT
15	206.5	13.1	417 1	WSL1_HUMAN
16	206	13.1	335 1	FASA_HUMAN
17	205	13.0	327 1	FASA_MOUSE
18	203.5	12.9	425 1	NGFR_RAT
19	200.5	12.7	323 1	FASA_BOVIN
20	198.5	12.6	416 1	NGFR_CHICK
21	194.5	12.3	277 1	OX40_HUMAN
22	192	12.2	461 1	TNR1_RAT
23	190	12.0	427 1	NGFR_HUMAN
24	176.5	11.2	256 1	ALBB_MOUSE
25	172.5	10.9	461 1	TNR1_PIG
26	171.5	10.9	471 1	TNR1_BOVIN
27	171	10.8	250 1	CD27_MOUSE
28	168.5	10.7	454 1	TNR1_MOUSE
29	161	10.2	255 1	ALBB_HUMAN
30	159	10.1	595 1	CD30_HUMAN
31	155	9.8	455 1	TNR1_HUMAN
32	148	9.4	260 1	CD27_HUMAN
33	143.5	9.1	1786 1	LMB1_HUMAN

34	133.5	8.5	4393 1	PGBM_HUMAN	P88160 homo sapien
35	130.5	8.3	1786 1	LMB1_MOUSE	P02469 mus musculus
36	127.5	8.1	3707 1	PGBM_MOUSE	O05793 mus musculus
37	126	8.0	1557 1	LM1L_CAEL	Q18823 caenorhabdi
38	126	8.0	1798 1	LMB2_HUMAN	P55268 homo sapien
39	125	7.9	722 1	DL1L_MOUSE	Q61483 mus musculus
40	122	7.7	714 1	DL1L_RAT	P97677 ratu mus norv
41	122	7.7	3106 1	LM42_MOUSE	O60675 mus musculus
42	121.5	7.7	1964 1	NTCA_MOUSE	P31695 mus musculus
43	121	7.7	755 1	COMP_RAT	P35444 ratu mus norv
44	120.5	7.6	1799 1	LMB2_MOUSE	O61292 mus musculus
45	118	7.5	1696 1	PCK5_BRACL	Q9nj15 branchiosto

ALIGNMENTS

```

RESULT 1
CD40_MOUSE STANDARD; PRT; 289 AA.
ID CD40_MOUSE
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BA1B/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC THE SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M83312; AAB08705.1; -
DR EMBL; M94126; AAA37404.1; -
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSP; P25942; 1CDF.
DR MGD; MGI:88336; Tnftrsf5.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.

```


Db 226 AP--HPKQFQEIHFPPDLPGSNTAPVQETL 255

RESULT 3
CD40_BOVIN STANDARD; PRT; 269 AA.
ID CD40_BOVIN
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
cattle.";
RT Immunology 90:294-300(1997).
RL -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: U57745; AAC48710.1; -
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 >269
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 23983 MW; 74690330F95F387 CRC64;

Query Match 16.9%; Score 267; DB 1; Length 269;
Best Local Similarity 28.0%; Pred. No. 7.7e-15;
Matches 65; Conservative 43; Mismatches 110; Indels 14; Gaps 5;

QY 20 VLRLVLYTLGLG---APCVAPALPSCKEDEYPVGSBCCPGKSGRYKRAAGELITGVCE 76
Db 1 MVRPLPLOCLEWGFLLTAHVSEPAACGEKQYVNSLCCDCLCPGQKLVNDCTEVSKTEQC 60
QY 77 PCPGRYIAHLNGLSKLOQCMQDPAMGLASNSCSTENAVGCGSGHICITQDDGHCA 136
Db 61 SCGKGELSTWNEKRYCHEHRNCPNGLRIQSEGLTLDITICVCEGQHC---TSHTCE 117

QY 137 ACRAVATSSGQRYQKGTESODTLCONCPGGTFS-PNGTLEEQHOTKCSML-VTKAGA 194
Db 118 SCPTSHSLCLPFGVQKQIATGLDITVCEPDLGFFSNSSAFKCHRWTSCEKGLVBOHV 177
QY 195 GTSSSHWMMWFSLGSLVIVICSTVGLICVKRRKPRGVDVKKVVSQRRKQ 246
Db 178 GTNKTDVYCGFQSGSMRTLVIVIPYTMGVFAVL-----VSACIRLITKKRQ 223

RESULT 4
VT2_SFVKA STANDARD; PRT; 325 AA.
ID VT2_SFVKA
AC P23943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
telomeric region of the Shope fibroma virus genome.";
RT Virology 160:20-30(1987).
RN [2]
RP MEDLINE=91207415; PubMed=1850261;
RX Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
form of the TNF receptor.";
RT Biochem. Biophys. Res. Commun. 176:335-342(1991).
RL -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M17433; -; NOT_ANNOTATED_CDS.
DR PIR: B43692; B43692.
DR HSSP: P19438; ITNR.
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 325
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 16.5%; Score 260; DB 1; Length 325;
 Best Local Similarity 31.5%; Pred. No. 3.4e-14;
 Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRLVLTFLGACVAPALP-----SCKEDFVPGSECCPKSPRYKACGELTGT 73
 DB 1 MLRIALLVCV-VVYVDVDPYSSNCKGCGHDEKDLCCASCHPGFYASRLCGPGSNT 59
 QY 74 VCEPCPGTIAHLNGLSKLCOCMPAMG-LRASRNCSTENAVCGSPGFHCIVODG 132
 DB 60 VCSCEGCTTASTNNAHAPACVSCR--GPGTGHSESPCDRTHDVNCSTGNTCLLKQ 117
 QY 133 DHCACRAVATSSPGQVQKGTESODTLQCNCPGTFSPN-GTLEDC-----179
 DB 118 NGCRIC-APQTKCPAGYGVGHFRAGDTLCEKCPHTYSDLSPTERCSTSPNYISVGFN 176
 QY 180----QHOKCSMLVTKAG 193
 DB 177 LYPVNETSCT--TTAG 190

RESULT 5
 TNR2_HUMAN STANDARD; PRT; 461 AA.
 ID TNR2_HUMAN
 AC P20333;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
 GN BINDING PROTEIN 2) (TNF1) (P80) (TNF-R2) (CD120B) (ETANERCEPT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90260639; PubMed-2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91045991; PubMed-2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96299745; PubMed-8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 33:94-100(1996).
 RN [4]
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-90349572; PubMed-216946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [5]
 RP SEQUENCE OF 27-31.
 RX MEDLINE-90110215; PubMed-2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface

RT tumor necrosis factor receptors.";
 RN J. Biol. Chem. 265:1531-1536(1990).
 RN [6]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE-91056048; PubMed-2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brocchhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE-93016040; PubMed-1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
 RX MEDLINE-99221490; PubMed-10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
 CC MYERH-AYERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
 CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
 CC WWW="http://www.enbrelinfo.com/".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M32315; AAA59929.1; -
 DR EMBL: M35857; AAA63262.1; -
 DR EMBL: U52165; AAC50622.1; -
 DR EMBL: U52165; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA6755.1; -
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNFR_c6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.

Query Match	16.4%	Score 259	DB 1:	Length 461
Best Local Similarity	32.8%	Pred. No. 5.6e-14		
Matches	59	Conservative	23	Mismatches 76
				Indels 22
				Gaps 6

RESULT	6		
VC22_VARV			
ID	VC22_VARV	STANDARD;	PRT;
	D3A015		349 AA

DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE PROTEIN C22/B28 HOMOLOG.
 GN GAR.
 OS Variola virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=INDIA-1967 / ISOLATE IND3;
 RX MEDLINE=93202281; PubMed=8384129;
 RA Shchelkunov S.N., Bilinov V.M., Sandakchchiev L.S.;
 RT "genes of variola and vaccinia viruses necessary to overcome the host
 RT protective mechanisms.";
 RL FEBS Lett. 319:80-83(1993).
 CC 1-1 SMILIARITY: COMPAIRNS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

Query Match	16.3%;	Score 257;	DB 1;	Length 349;
Best Local Similarity	29.3%;	Pred. No. 6, 3e-14;		
Matches 66;	Conservative 23;	Mismatches 94;	Indels 42;	Gaps 8;

RESULT	7		
TNRC_HUMAN			
ID	TNRC_HUMAN	STANDARD;	PRT; 435 AA
NC	P36041.		

DT 01-JUN-1994 (Rel. 29, created)
 DT 01-JUN-1994 (Rel. 29, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
 GN LTR OR TNFR OR TNFRSF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RT Beens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.,
 RT "Construction and evaluation of a hncDNA library of human 12p
 RT transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., van Asdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,
 RA "A lymphotoxin-beta specific receptor.";
 RL Science 264:707-710(1994).

```

CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L04270; AAA36757.1; -.
CC HSSP: P25942; ICDF.
CC MIM: 600979; -.
CC InterPro: IPR001368; -.
CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE: PS50050; TNFR_NGFR_2; 3.
CC KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
CC -----
CC CHAIN 1 30 POTENTIAL.
CC FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
CC FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 228 248 POTENTIAL.
CC FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 42 211 4 X TNFR-CYS.
CC FT REPEAT 42 81 TNFR-CYS 1.
CC FT REPEAT 82 124 TNFR-CYS 2.
CC FT REPEAT 125 168 TNFR-CYS 3.
CC FT REPEAT 169 211 TNFR-CYS 4.
CC FT DISULFID 43 58 BY SIMILARITY.
CC FT DISULFID 59 72 BY SIMILARITY.
CC FT DISULFID 62 80 BY SIMILARITY.
CC FT DISULFID 83 98 BY SIMILARITY.
CC FT DISULFID 101 116 BY SIMILARITY.
CC FT DISULFID 104 124 BY SIMILARITY.
CC FT DISULFID 126 132 BY SIMILARITY.
CC FT DISULFID 139 148 BY SIMILARITY.
CC FT DISULFID 142 167 BY SIMILARITY.
CC FT DISULFID 170 185 BY SIMILARITY.
CC FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 435 AA; 46709 MW; 624626B6022F656F CRC64;

```

```

RESULT 8
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LYBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nakarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U29173; AAA68964.1; -.
CC DR EMBL: L38423; AAB00846.1; -.
CC DR EMBL: U30798; AAA81334.1; -.
CC DR HSSP: P25942; ICDF.
CC DR MGD: MGI:104875; ltblr.
CC DR InterPro: IPR001368; -.
CC DR Pfam: PF00020; TNFR_C6; 3.
CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE: PS50050; TNFR_NGFR_2; 3.
CC KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
CC -----
CC CHAIN 1 30 POTENTIAL.
CC FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
CC FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 224 244 POTENTIAL.
CC FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 42 213 4 X TNFR-CYS.
CC FT REPEAT 42 81 TNFR-CYS 1.
CC FT REPEAT 82 124 TNFR-CYS 2.
CC FT REPEAT 125 170 TNFR-CYS 3.
CC FT REPEAT 171 213 TNFR-CYS 4.
CC FT DISULFID 43 58 BY SIMILARITY.
CC FT DISULFID 59 72 BY SIMILARITY.
CC FT DISULFID 62 80 BY SIMILARITY.
CC FT DISULFID 83 98 BY SIMILARITY.
CC FT DISULFID 101 116 BY SIMILARITY.
CC FT DISULFID 104 124 BY SIMILARITY.
CC FT DISULFID 126 132 BY SIMILARITY.
CC FT DISULFID 139 150 BY SIMILARITY.

```


FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 15.6%; Score 245.5; DB 1; Length 415;
 Best Local Similarity 25.9%; Pred. No. 6.3e-13;
 Matches 83; Conservative 40; Mismatches 115; Indels 83; Gaps 15;

QY 7 WGP-----PWRSTPRTDYLRLVLYLTFGAPCYAPALPSCKEDY-- 47
 DB 14 WGPLLGLSLVLSQPOLVPPRYENOT-----CWD-----ODKEYE 52
 QY 48 PVGSCPCPKSPGYRVKACGELGTVCPCPPGTIYIAHLNGLSKLCLOQCMCDPAMGLRA 107
 DB 53 PMHVCSCRCPPGEFVAVGSRSDTVCCTPHNSYNEHMHSLTQCLCRPDIVLGFEE 112
 QY 108 SRNCSRTENAVCGSPGHFCIVODGD--HCAACRAVATSSPGORVOKGSTESQ----- 158
 DB 113 VAPCTSDKACRCQPGMCSYVLDNECVHCEERLY-----LCQGTAEVYDEIMD 164
 QY 159 -DTLCQNCPPGT--SPNGTLECCQHOTKCSML-VTKAGAGTSSSHW----- 202
 DB 165 TDVNCVPCPKPHFQNTSSPRA---RCOPHTRCLEIQLGLVEAPGTSYDPTICKNPPPGAM 221
 QY 203 -WPFSLVLYVICSPTGLICVKKRRKRDYKVIYSORKRQEAEGATVIEALQAP 261
 DB 222 LLALILSLVFLFTY--LACAMMRHP--SLCKRLGLTKRHEGE-ESPPCAPAPAD 276
 QY 262 PDVTVAVETPTSPFTGRSPN 282
 DB 277 PHFPDLA-EPLLPMSGDLSPS 296

RESULT 9

OX40_RAT STANDARD; PRT; 271 AA.
 ID OX40_RAT
 AC P15725;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
 GN TNFRSF4 OR TRXPL1 OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90214614; PubMed=2157591;
 RA Mallett S., Fossum S., Barclay A.N.;
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
 lymphocytes -- a molecule related to nerve growth factor receptor.";
 RL EMO J. 9:1063-1068(1990).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: X17037; CA34897.1; -
 DR PIR: S08036; S08036.
 DR PIR: S12783; S12783.

DR HSSP; P25942; 1CDF.
 DR InterPro; IPR001368; -
 DR Pfam; PF00020; TNFR_c6; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
 FT SIGNAL 1 19
 FT CHAIN 20 271
 FT DOMAIN 20 210
 FT TRANSMEM 211 235
 FT DOMAIN 236 271
 FT DOMAIN 25 164
 FT REPEAT 25 60
 FT REPEAT 61 102
 FT REPEAT 103 123
 FT REPEAT 124 164
 FT CARBOHYD 143 143
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 15.2%; Score 240.5; DB 1; Length 271;
 Best Local Similarity 34.9%; Pred. No. 1.1e-12;
 Matches 51; Conservative 16; Mismatches 54; Indels 25; Gaps 5;

QY 41 SCKDEYFVGSCECPKSPGYRVKACGELGTVCPCPPGTIYIAHLNGLSKLCLOQCMCD 100
 DB 25 NCVADTYPSGKCCRECPGHSMSRCDHTDYCHCPGPFYMAVN-YPTQACQYCN 83
 QY 101 PAMGLRSRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGSTESODT 160
 DB 84 HRSGSELKQNTPTEDYVQCRRPG--TOPRODSSH-----KLQVD----- 121
 QY 161 LCQNCPPGTSPNGTLECCQHOTKCS 186
 DB 122 -CVPCPPGHFSP-GSNACKPWTNCT 145

RESULT 10

VT2_MXVXL STANDARD; PRT; 326 AA.
 ID VT2_MXVXL
 AC P29825;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS Myxoma virus (strain Lausanne).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 OX NCBI_TaxID=31530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9135768; PubMed=1651597;
 RA Upton C., Macen J.L., Schreiber M., McFadden G.;
 RT "Myxoma virus expresses a secreted protein with homology to the tumor
 RT necrosis factor receptor gene family that contributes to viral
 RT virulence.";
 RL Virology 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: M95181; AAA46632.1; -
 DR -----

DR EMBL: A23729; CA01688.1; -
 DR PIR: A40566; GOVZML.
 DR HSSP: P19438; 1TNR.
 DR InterPro: IPR001368; -
 DR Pfam: PF00020; TNR_C6; 2.
 DR PROSITE: PS00652; TNR_NGFR_1; 2.
 DR PROSITE: PS50050; TNR_NGFR_2; 2.
 DR Receptor: Glycoprotein; Repeat; Signal.
 DR SIGNAL: 16
 FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
 FT DOMAIN 27 186 4 X TNR-CYS.
 FT REPEAT 27 62 TNR-CYS 1.
 FT REPEAT 63 104 TNR-CYS 2.
 FT REPEAT 105 147 TNR-CYS 3.
 FT REPEAT 148 186 TNR-CYS 4.
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 35208 MW; ABBF027B947292PF CRC64;

Query Match 15.18; Score 238.5; DB 1; Length 326;
 Best Local Similarity 26.84; Pred. No. 1.9e-12;
 Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;

QY 20 VLRLVLYFLP-----GAPCYALPSPCKEDEVSECCPKSPGYRYKACGELTGT 73
 DB 1 MFRITLLAVACYGGAP-YGADRGRCKRNDYERKGLCTSPSPSYASRLCGPSDT 59
 QY 74 VCEPCPGTYIAHLNGLSKLQCO-MCDPAMGLASRNCSTENAVGCGSPGHFCIVODG 132
 DB 60 VCSCKNETFTASTNHAAPACVSCRGRC--TGHLSQSQCSDTRVOCDSNGNYCLKGO 117
 QY 133 DHACAGATATSSGQVQKGTESODTLQONCPGFSPN-GLLECO----- 180
 DB 118 EGKRIC-APTKCPAGYGVSGHRTGDLCTKCPRTYSDAVSSTECTSSFNYSVEFN 176
 QY 181 ----HOTKCSWLVRKGA-----GTSSSHWMMFLSGS 209
 DB 177 LYPNDTSC---TTAGPNEVKTSEFSVLNHTDCDPVFHTETGYTSGSGAGGFTTGM 233
 QY 210 ---LVIVICSTVGLIICVKKRPRGDVYKVI 238
 DB 234 DRYONTKMTCLNIEIRCV-----GDAVRTI 260

RESULT 11

FASA_PIG STANDARD; PRT; 332 AA.
 AC 077736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 OS TNFRSF6 OR APT1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCBL_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT Expression of apoptosis-associated genes in hibernating and stunned
 RT myocardium of pig.;
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING

CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: A001202; CA04596.1; -
 DR InterPro: IPR00488; -
 DR InterPro: IPR001368; -
 DR Pfam: PF00531; death: 1.
 DR PROSITE: PS00652; TNR_NGFR_1; 2.
 DR PROSITE: PS50050; TNR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 DR SIGNAL: 16
 FT CHAIN 17 332
 FT DOMAIN 17 175
 FT TRANSMEM 176 192
 FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 45 164 3 X TNR-CYS.
 FT REPEAT 45 81 TNR-CYS 1.
 FT REPEAT 82 125 TNR-CYS 2.
 FT REPEAT 126 164 TNR-CYS 3.
 FT DOMAIN 227 311 DEATH DOMAIN.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 332 AA; 37592 MW; 58B803682756BF1B CRC64;

Query Match 15.08; Score 236; DB 1; Length 332;
 Best Local Similarity 27.54; Pred. No. 3e-12;
 Matches 65; Conservative 30; Mismatches 95; Indels 46; Gaps 9;

QY 42 CKDEYVPGSECCPKSPGYRYKACGELTGT-VCEPCPG-TYIAHLNGLSKLQCO 99
 DB 46 CPEQHQREGQFCQPCPPGRKHADCTSPGAPQCVCSGEGDTYDKNHSSKRCRCVC 105
 QY 100 DPMGLASRNCSTENAVGCGSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESOD 159
 DB 106 DSGHGLEVENKTRIQNTQKRCRKNPFCHSQCCEHCPC----- 144
 QY 160 TLQONCPGTFSPNGTLEEC--OHOTKCSWLVRKAGAGTSSSHWMMFLSGSLVIYVCS 217
 DB 145 TTCE-----HGVIENTPTSPNCREVFQASG-RSNLLMLW---ALLILPVPA 190
 QY 218 TVGLIICVKKRPRGDVYIVSVQKROEAGEATVIELQAPPDVTVAVEETI 273
 DB 191 LVYREVKRRCRKRENGYKPTTS-----NAE-EVPMIKIVDLGKYYITRAEQMKI 239

RESULT 12

OX40_MOUSE STANDARD; PRT; 272 AA.
 ID OX40_MOUSE
 AC P47741;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
 GN TNFRSF4 OR TXGP1 OR OX40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN TNFRSF6 OR P11 OR FAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurgnathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=9412814; PubMed=7507668;
RA Kimura K., Yamamoto M., Wakatsuki T.;
RT "A variant mRNA species encoding a truncated form of Fas antigen in
the rat liver.";
RL Biochem. Biophys. Res. Commun. 198;666-674(1994).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC Cysteine PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS A LA-NER/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

RESULT	15	WSL1_HUMAN	STANDARD:	PRT:	417 AA.
ID	WSL1_HUMAN				
AC	Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;				
AC	Q99830; Q99830; 1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)				
DE	(APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH) (LARD).				
DE	TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.				
GN	Homo sapiens (Human).				
OS	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
ON	[1]				

[illegible]

Search completed: April 25, 2001, 17:36:13
Job time: 99 sec